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OM protein - protein search, using sw model

Run on: January 28, 2005, 21:56:43 ; Search time 33.3149 Seconds  
(without alignments)  
816.164 Million cell updates/sec

Title: US-09-918-715-230\_COPY\_18\_427

Perfect score: 2218  
Sequence: 1 ALSPPQAGHDEGPGSWAA.....GLQNNLSPKYKGPVHLGTI 410

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.\*

1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*

2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*

3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*

4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*

5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*

6: /cgn2\_6/ptodata/1/iaa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1795	80.9	431	4	US-09-912-935-36
2	1066.5	48.1	499	4	US-09-912-935-31
3	1066.5	48.1	529	4	US-09-912-935-28
4	1066.5	48.1	529	4	US-09-912-935-40
5	1055	47.6	449	4	US-09-912-935-34
6	1047.5	47.2	425	4	US-09-912-935-35
7	1044	47.1	530	4	US-09-912-935-38
8	948	42.7	392	4	US-09-764-325A-23
9	948	42.7	392	4	US-09-764-325A-25
10	948	42.7	392	4	US-09-912-935-23
11	948	42.7	392	4	US-09-912-935-25
12	115.5	5.2	1568	3	US-09-181-706-2
13	115.5	5.2	1568	3	US-09-458-791-2
14	115.5	5.2	1568	3	US-09-459-066-2
15	115.5	5.2	1568	4	US-09-459-065-2
16	97	4.4	712	4	US-09-543-681A-6132
17	93.5	4.2	1977	4	US-09-976-594-757
18	93.5	4.2	1977	4	US-09-919-039-367
19	93	4.2	1085	1	US-08-431-080-28
20	93	4.2	1085	2	US-08-938-534-28
21	93	4.2	1085	3	US-09-345-294-28
22	92.5	4.2	1220	1	US-08-158-232-43
23	92.5	4.2	1220	2	US-08-611-928-43
24	92.5	4.2	1220	3	US-09-173-891-43
25	89.5	4.0	424	6	5169835-6
26	89.5	4.0	446	4	US-09-252-991A-31114
27	89	4.0	517	4	US-09-248-796A-14652

28	88	4.0	606	3	US-09-041-236-4	Sequence 4, Appli
29	88	4.0	606	4	US-09-771-467C-4	Sequence 4, Appli
30	87.5	3.9	1969	3	US-08-836-325-16	Sequence 16, Appl
31	87.5	3.9	1969	4	US-09-457-571-16	Sequence 16, Appl
32	87	3.9	362	4	US-09-252-991A-31349	Sequence 31349, A
33	86.5	3.9	518	4	US-09-816-248-17	Sequence 17, Appl
34	86.5	3.9	577	4	US-09-489-039A-13973	Sequence 13973, A
35	85.5	3.9	284	2	US-08-424-641B-2	Sequence 2, Appli
36	85.5	3.9	284	2	US-08-820-980-2	Sequence 2, Appli
37	85.5	3.9	284	2	US-08-826-439-2	Sequence 2, Appli
38	85.5	3.9	349	3	US-09-161-241-8	Sequence 8, Appli
39	85.5	3.9	597	4	US-09-248-796A-14379	Sequence 14379, A
40	84.5	3.8	490	4	US-09-461-325-250	Sequence 250, App
41	84.5	3.8	490	4	US-09-461-325-518	Sequence 518, App
42	84.5	3.8	490	4	US-10-012-542-250	Sequence 518, App
43	84.5	3.8	490	4	US-10-012-542-518	Sequence 518, App
44	84.5	3.8	490	4	US-10-115-123-250	Sequence 250, App
45	84.5	3.8	490	4	US-10-115-123-518	Sequence 518, App

#### ALIGNMENTS

RESULT 1  
US-09-912-935-36  
; Sequence 36, Application US/09912935  
; Patent No. 6673904  
; GENERAL INFORMATION:  
; APPLICANT: Nishikawa, Mitsuo et al.  
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE  
; FILE REFERENCE: 32066/37483  
; CURRENT APPLICATION NUMBER: US/09/912.935  
; CURRENT FILING DATE: 2001-07-24  
; PRIOR APPLICATION NUMBER: PCT/US00/35260  
; PRIOR FILING DATE: 2000-12-23  
; NUMBER OF SEQ ID NOS: 53  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 36  
; LENGTH: 431  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-912-935-36

Query Match 80.9%; Score 1795; DB 4; Length 431;

Best Local Similarity 94.2%; Pred. No. 1.7e-168;

Matches 343; Conservative 0; Mismatches 7; Indels 14; Gaps 3;

Qy	55	LAMDTLPDNRTRVVEDNHSYVSRLYGSPSPHRELWVDVAENRSQVKIHTILSNTRQ	114
Db	1	LAMDTLPDNRTRVVEDNHSYVSRLYGSPSPHRELWVDVAENRSQVKIHTILSNTRQ	60
Qy	115	ASRVVLSFDRPFYGHPLRQITATGGTFMCGDVHRLMTATQYVAPLMANFNPGYSDNST	174
Db	61	ASRVVLSFDRPFYGHPLRQITATGGTFMCGDVHRLMTATQYVAPLMANFNPGYSDNST	120
Qy	175	VVYFDNGTFVYVQNDHVLQGMEDKGSFTFOAALHHDGRIVFYAYKEIPMSVPEISSQHP	234
Db	121	VVYFDNGTFVYVQNDHVLQGMEDKGSFTFOAALHHDGRIVFYAYKEIPMSVPEISSQHP	180
Qy	235	VKTGLSDFAMFLNPSDPVPSRRRSIFHYHRIELDPKSVTMSAVEFTPLTCLQHRSD	294
Db	181	VKTGLSDFAMFLNPSDPVPSRRRSIFHYHRIELDPKSVTMSAVEFTPLTCLQHRSD	240
Qy	295	ACMSDDLTFCNSWCHVLCQRCSSGFRYQEW-MDYGCAQAEGRMCEDFQD-----ED	346
Db	241	ACMSDDLTFCNSWCHVLCQRCSSGFRYQEWMDGTGCAQAEAG-----QDVRGLPGHRT	294
Qy	347	HDSASPTSFSPYDGLTTTSSSLFIDSLTATDDTKLNPYAGGDLQNNLSPKTKGTPVH	406
Db	295	TTSASPTSFSPYDGLTTTSSSLFIDSLTATDDTKLNPYAGGDLQNNLSPKTKGTPVH	354
Qy	407	LGTI 410	



Db 215 TVRYFDNGTALVQWDHVLQDNYLGSFTFOATLLMDGRIIFGYKEIPVLVTQISSTNH 274  
Qy 234 PVKGLSDFMLNPSDPVPSRRSIEFYHRIELDPKSVTSMASAVEFTPLTCLQHRSC 293  
Db 275 PVKGLSDFMLNPSDPVPSRRSIEFYHRIELDPKSVTSMASAVEFTPLTCLQHRSC 334  
Qy 294 DACMSSDLTFNCSCHVLQRCSSGFDYRQEMDYGCAEAGRCMCEFDQEDHDSASPD 353  
Db 335 GPCVSSQIGFNCSCWKLQRCSSGFDYRQEMDYGCAEAGRCMCEFDQEDHDSASPD 394  
Qy 354 T--SFSPYDGLTTS---SSLFIDSLTETDQKLNYPAGGDLQ--NNLSPKTKGTPVHL 407  
Db 395 TVGATTTQFRVLTTTTRRAVTSQFTSLPTEDDTKIALHLKONGASTDDSAAEKGGTLHA 454  
Qy 408 GTI 410  
Db 455 GLI 457

## RESULT 5

US-09-912-935-34  
; Sequence 34, Application US/09912935  
; Patent No. 6673904  
; GENERAL INFORMATION:  
; APPLICANT: Nishikawa, Mitsuo et al.  
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE  
; FILE REFERENCE: 32066/37483  
; CURRENT APPLICATION NUMBER: US/09/912,935  
; CURRENT FILING DATE: 2001-07-24  
; PRIOR APPLICATION NUMBER: PCT/US00/35260  
; PRIOR FILING DATE: 2000-12-23  
; NUMBER OF SEQ ID NOS: 53  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 34  
; LENGTH: 449  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-912-935-34

Query Match 47.6%; Score 1055; DB 4; Length 449;

Best Local Similarity 57.2%; Pred. No. 2e-95;  
Matches 202; Conservative 59; Mismatches 86; Indels 6; Gaps 3;

Qy 55 LAMDTLPDNRTRVVED--NHSYVYVRLYGPSPHSELVAVAEANRSQVKIHTILSNTHR 113  
Db 95 LLDGQDNNTQIEDTTHNYIIRIYGPSSASRDLWNIDQMEKDKVKIHGILSNTHR 154  
Qy 114 QASRVLSDFPPFYGHPLRQITATGGFIEMGDVIRHMLTATQYVAPLMAFNPFGYSDNS 173  
Db 155 QAARVNLSDFFPYGHFLREITVATGGFIYTGVEVVRHMLTATQYIAPLMAFNPFSVRNS 214  
Qy 174 TVVYFDNGTALVQWDHVLQDNYLGSFTFOATLLMDGRIIFGYKEIPVLVTQISSTNH 233  
Db 215 TVRYFDNGTALVQWDHVLQDNYLGSFTFOATLLMDGRIIFGYKEIPVLVTQISSTNH 274  
Qy 234 PVKGLSDFMLNPSDPVPSRRSIEFYHRIELDPKSVTSMASAVEFTPLTCLQHRSC 293  
Db 275 PVKGLSDFMLNPSDPVPSRRSIEFYHRIELDPKSVTSMASAVEFTPLTCLQHRSC 334  
Qy 294 DACMSSDLTFNCSCHVLQRCSSGFDYRQEMDYGCAEAGRCMCEFDQEDHDSASPD 353  
Db 335 GPCVSSQIGFNCSCWKLQRCSSGFDYRQEMDYGCAEAGRCMCEFDQEDHDSASPD 394  
Qy 354 T--SFSPYDGLTTS---SSLFIDSLTETDQKLNYPAGGDLQ--NNLSPKTKGTPVHL 407  
Db 395 TVGATTTQFRVLTTTTRRAVTSQFTSLPTEDDTKIALHLKONGASTDDSAAEKGGTLHA 447

## RESULT 6

US-09-912-935-35  
; Sequence 35, Application US/09912935

; Patent No. 6673904  
; GENERAL INFORMATION:  
; APPLICANT: Nishikawa, Mitsuo et al.  
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE  
; FILE REFERENCE: 32066/37483  
; CURRENT APPLICATION NUMBER: US/09/912,935  
; CURRENT FILING DATE: 2001-07-24  
; PRIOR APPLICATION NUMBER: PCT/US00/35260  
; PRIOR FILING DATE: 2000-12-23  
; NUMBER OF SEQ ID NOS: 53  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 35  
; LENGTH: 425  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-912-935-35

Query Match 47.2%; Score 1047.5; DB 4; Length 425;

Best Local Similarity 56.9%; Pred. No. 1e-94;  
Matches 203; Conservative 55; Mismatches 88; Indels 11; Gaps 4;

Qy 61 PDNRTRVVEDNHSYVYVRLYGPSPHSELVAVAEANRSQVKIHTILSNTHRQASRVVL 120  
Db 1 PRVRPRVRTD--HNYIIRIYGPSSASRDLWNIDQMEKDKVKIHGILSNTHRQAAVNML 59  
Qy 121 SFDPPFYGHPLRQITATGGFIEMGDVIRHMLTATQYVAPLMAFNPFGYSDNSTVYFDN 180  
Db 60 SFDPPFYGHFLREITVATGGFIYTGVEVVRHMLTATQYIAPLMAFNPFSVRNSTVYFDN 119  
Qy 181 GTVFWQMDHVLQGWEDKGSFTFOALHHDGRIVFAYKEIPMSVPEISSQHPVKTGLS 240  
Db 120 GTALVQWDHVLQDNYLGSFTFOATLLMDGRIIFGYKEIPVLVTQISSTNHPVKVGLS 179  
Qy 241 DAFMLNPSDPVPSRRSIEFYHRIELDPKSVTSMASAVEFTPLTCLQHRSCDCMSSD 300  
Db 180 DAFVVRHRIQIIPNRRRTIYHVRVQLQMSKITNISAVEMTPLTCLQHRSCGCVSSQ 239  
Qy 301 LTFNCSCHVLQRCSSGFDYRQEMDYGCAEAGRCMCEFDQEDHDSASPD 354  
Db 240 IGFNCSCKLQRCSSGFDYRQEMDYGCAEAGRCMCEFDQEDHDSASPD 299  
Qy 355 SFSYDGLTTS--SSLFIDSLTETDQKLNYPAGGDLQ--NNLSPKTKGTPVHLGTI 410  
Db 300 SGSLPPEDAVT---SQFPTSLPTEDDTKIALHLKONGASTDDSAAEKGGTLHAGLI 353

## RESULT 7

US-09-912-935-38  
; Sequence 38, Application US/09912935  
; Patent No. 6673904  
; GENERAL INFORMATION:  
; APPLICANT: Nishikawa, Mitsuo et al.  
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE  
; FILE REFERENCE: 32066/37483  
; CURRENT APPLICATION NUMBER: US/09/912,935  
; CURRENT FILING DATE: 2001-07-24  
; PRIOR APPLICATION NUMBER: PCT/US00/35260  
; PRIOR FILING DATE: 2000-12-23  
; NUMBER OF SEQ ID NOS: 53  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 38  
; LENGTH: 530  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-912-935-38

Query Match 47.1%; Score 1044; DB 4; Length 530;

Best Local Similarity 51.3%; Pred. No. 3.2e-94;  
Matches 203; Conservative 67; Mismatches 112; Indels 14; Gaps 6;

Qy 27 WNRRAESPGRVHSEPDRTQLSQ-----DLGGGTGLAMDTLPDNRTRVVED--NHSYVYVRLYG 81

Db 65 WKRV--DPPRAVDNTRASMGQSPESKGFDTLLDDQDNNNTQIEEDTDHNYISRYG 122  
Qy 82 PSBHSRLWVDVAEANRSQVKIHTLSNTHROASRVVLSDFDPFPGYHPLRQIATGGF 141  
Db 123 PADSASRLWNIIDQEMDKVKIHLNTHROARVNLSPDFPGYHPLNEVTVATGGF 182  
Qy 142 IFMGDVHRLMTATQYVAPLANFNPVGYSDNSTVYFDNGTVFVQVMDHVYVQWEDKGS 201  
Db 183 IYTGVEVHRMTATQYIAPLANFNPVGYSDNSTVYFDNGTVFVQVMDHVYVQWEDKGS 242  
Qy 202 FTFOALHHDGRIVFAYKEIPMSVPEISSQHPVKTLGSLDAPMLNPSDPVPESSRSIF 261  
Db 243 FTFOATLLMDGRIIFGYKEIPVLTQISSTNHPVKVGLSDAFVVRHRIQQIPNVRRIT 302  
Qy 262 EYHRIELDPKVTMSAVEFTPLTCLQHRSCDACMSDLTFNCSGCHVLRQCSGDFRY 321  
Db 303 EYHRELQMSKITNISAVEMTPLTCLQFNGCGPCVSSQIGFNCSSKLRQCSGDFRH 362  
Qy 322 ROEMNDYCAEAG--RMCEDFQDEHDSASPTSPSPYDGLTTS---SSLFIDSL 375  
Db 363 RQDWVDSGCPBEVQSKCKMCKBETGETSQTTTSHITMQFRVLTITRRRAVTSQMTSL 422  
Qy 376 TTEDDTKLNYPAGDGLQ--NNLSPKTKGTPVHLGTI 410  
Db 423 PTEDDTKIALHLKDSGASTDSDAAEKKGGTLHAGLI 458

## RESULT 8

US-09-764-325A-23  
; Sequence 23, Application US/09764325A  
; Patent No. 6667391  
; GENERAL INFORMATION:  
; APPLICANT: Labat, Ivan  
; APPLICANT: Drmanac, Radoje T.  
; APPLICANT: Tang, Y. T.  
; APPLICANT: Chao, Cheng-Chi  
; APPLICANT: Mize, Nancy K.  
; APPLICANT: Childs, John  
; TITLE OF INVENTION: Methods and Materials Relating to No. 6667391el Stem Cell  
; FILE REFERENCE: 30266/37630A  
; CURRENT APPLICATION NUMBER: US/09/764,325A  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: 09/547,358  
; PRIOR FILING DATE: 2000-04-11  
; PRIOR APPLICATION NUMBER: 09/545,714  
; PRIOR FILING DATE: 2000-04-07  
; PRIOR APPLICATION NUMBER: 09/488,725  
; PRIOR FILING DATE: 2000-01-21  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 23  
; LENGTH: 392  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-764-325A-23

Query Match 42.7%; Score 948; DB 4; Length 392;  
Best Local Similarity 57.9%; Pred. No. 6e-85;  
Matches 184; Conservative 51; Mismatches 77; Indels 6; Gaps 3;

Qy 99 RSQVKIHTLSNTHROASRVVLSDFDPFPGYHPLRQIATGGFIPMGDVHRLMTATQYV 158  
Db 3 KDKVKIHGILSNTHROARVNLSPDFPGYHPLRQIATGGFIVTGEVHRMLTATQYI 62  
Qy 159 APLMANFNPVGYSDNSTVYFDNGTVFVQVMDHVYVQWEDKGSFTFOALHHDGRIVP 218  
Db 63 APLMANFNPVGYSDNSTVYFDNGTVFVQVMDHVYVQWEDKGSFTFOALHHDGRIVP 122  
Qy 219 KEIPMSVPEISSQHPVKTLGSLDAPMLNPSDPVPESSRSIFEVHRIELDPKVTMSA 278  
Db 123 KEIPVLTQISSTNHPVKVGLSDAFVVRHRIQQIPNVRRITIEYHRELQMSKITNISA 182

Qy 279 VEFTPLTCLQHRSCDACMSDLTFNCSGCHVLRQCSGDFRYQEMNDYCAEAGRM 338  
Db 183 VEMTPLTCLQFNGCGPCVSSQIGFNCSSKLRQCSGDFRHQDWVDSGCPESKEKM 242  
Qy 339 CEDFQDEHDSASPT--SFPYDGLTTS---SSLFIDSLTTEDDTKLNYPAGDGLQ 393  
Db 243 CENTPEVTSRRTTTTGATTTQFRVLTITRRRAVTSQPTSLPTEDDTKIALHLKDNAS 302  
Qy 394 --NNLSPKTKGTPVHLGTI 410  
Db 303 TDDSAAEKKGGTLHAGLI 320

## RESULT 9

US-09-764-325A-25  
; Sequence 25, Application US/09764325A  
; Patent No. 6667391  
; GENERAL INFORMATION:  
; APPLICANT: Labat, Ivan  
; APPLICANT: Drmanac, Radoje T.  
; APPLICANT: Tang, Y. T.  
; APPLICANT: Chao, Cheng-Chi  
; APPLICANT: Mize, Nancy K.  
; APPLICANT: Childs, John  
; TITLE OF INVENTION: Methods and Materials Relating to No. 6667391el Stem Cell  
; FILE REFERENCE: 30266/37630A  
; CURRENT APPLICATION NUMBER: US/09/764,325A  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: 09/547,358  
; PRIOR FILING DATE: 2000-04-11  
; PRIOR APPLICATION NUMBER: 09/545,714  
; PRIOR FILING DATE: 2000-04-07  
; PRIOR APPLICATION NUMBER: 09/488,725  
; PRIOR FILING DATE: 2000-01-21  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 25  
; LENGTH: 392  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-764-325A-25

Query Match 42.7%; Score 948; DB 4; Length 392;  
Best Local Similarity 57.9%; Pred. No. 6e-85;  
Matches 184; Conservative 51; Mismatches 77; Indels 6; Gaps 3;

Qy 99 RSQVKIHTLSNTHROASRVVLSDFDPFPGYHPLRQIATGGFIPMGDVHRLMTATQYV 158  
Db 3 KDKVKIHGILSNTHROARVNLSPDFPGYHPLRQIATGGFIVTGEVHRMLTATQYI 62  
Qy 159 APLMANFNPVGYSDNSTVYFDNGTVFVQVMDHVYVQWEDKGSFTFOALHHDGRIVP 218  
Db 63 APLMANFNPVGYSDNSTVYFDNGTVFVQVMDHVYVQWEDKGSFTFOALHHDGRIVP 122  
Qy 219 KEIPMSVPEISSQHPVKTLGSLDAPMLNPSDPVPESSRSIFEVHRIELDPKVTMSA 278  
Db 123 KEIPVLTQISSTNHPVKVGLSDAFVVRHRIQQIPNVRRITIEYHRELQMSKITNISA 182  
Qy 279 VEFTPLTCLQHRSCDACMSDLTFNCSGCHVLRQCSGDFRYQEMNDYCAEAGRM 338  
Db 183 VEMTPLTCLQFNGCGPCVSSQIGFNCSSKLRQCSGDFRHQDWVDSGCPESKEKM 242  
Qy 339 CEDFQDEHDSASPT--SFPYDGLTTS---SSLFIDSLTTEDDTKLNYPAGDGLQ 393  
Db 243 CENTPEVTSRRTTTTGATTTQFRVLTITRRRAVTSQPTSLPTEDDTKIALHLKDNAS 302  
Qy 394 --NNLSPKTKGTPVHLGTI 410  
Db 303 TDDSAAEKKGGTLHAGLI 320



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RESULT 10
US-09-912-935-23
; Sequence 23, Application US/09912935
; Patent No. 6673904
; GENERAL INFORMATION:
; APPLICANT: Nishikawa, Mitsuo et al.
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
; FILE REFERENCE: 32066/37483
; CURRENT APPLICATION NUMBER: US/09/912,935
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: PCT/US00/35260
; PRIOR FILING DATE: 2000-12-23
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 23
; LENGTH: 392
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-912-935-23

Query Match 42.7%; Score 948; DB 4; Length 392;
Best Local Similarity 57.9%; Pred. No. 6e-85;
Matches 184; Conservative 51; Mismatches 77; Indels 6; Gaps 3;

QY 99 RSQVKIHTLSNTHRQASRVVLSDFPFYGHPLRQITTIATGCFIPMGDVIHRLMTATQYV 158
DB 3 KDKVKIHGILSNTHRQAAVNLSDFPFYGHPLRQITTIATGCFIYTGVEVHRLMTATQYI 62
QY 159 APLMANFPGVSDNSTVYFNGTGVVQVQVHVLQGWEDKGSFTFOALHHDGRIVPAY 218
DB 63 APLMANFPGVSRNSTVRYFNGTGVVQVQVHVLQGWEDKGSFTFOALHHDGRIVPAY 122
QY 219 KEIPMSVPEISSOHVPKTVGLSDAFMLNPSDPVPESSRSIFEVHRIELDPKSVTMSA 278
DB 123 KEIPVLVTQISSTNHPVKVGLSDAFVVRHRTQQIPNVRRRTIYEVHVELQMSKITNISA 182
QY 279 VEFTPLPTCLQHRSCDACMSSDLTFNCVCHVLRQCSSGDFRQYRQEWMDYCAQAEGRM 338
DB 183 VEMTPLPTCLQFNRGCGPCVSSQIGFNCVCHVLRQCSSGDFRQYRQEWMDYCAQAEGRM 242
QY 339 CEDFQDEHDSASPD--SFPYDGLTTS---SSLFIDSLTTEDDTKLPYAGDGLQ 393
DB 243 CENTPEVETSSRTTTTIGATTQFRVLTTRRAVTSQPTSLPTEDDTKIALHLKDNAS 302
QY 394 -NLSPKTKGTPVHLGTI 410
DB 303 TDDSAEKKGGTLLHAGLI 320

RESULT 11
US-09-912-935-25
; Sequence 25, Application US/09912935
; Patent No. 6673904
; GENERAL INFORMATION:
; APPLICANT: Nishikawa, Mitsuo et al.
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
; FILE REFERENCE: 32066/37483
; CURRENT APPLICATION NUMBER: US/09/912,935
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: PCT/US00/35260
; PRIOR FILING DATE: 2000-12-23
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 25
; LENGTH: 392
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-912-935-25

Query Match 42.7%; Score 948; DB 4; Length 392;
Best Local Similarity 57.9%; Pred. No. 6e-85;
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Matches 184; Conservative 51; Mismatches 77; Indels 6; Gaps 3;

QY 99 RSQVKIHTLSNTHRQASRVVLSDFPFYGHPLRQITTIATGCFIPMGDVIHRLMTATQYV 158
DB 3 KDKVKIHGILSNTHRQAAVNLSDFPFYGHPLRQITTIATGCFIYTGVEVHRLMTATQYI 62
QY 159 APLMANFPGVSDNSTVYFNGTGVVQVQVHVLQGWEDKGSFTFOALHHDGRIVPAY 218
DB 63 APLMANFPGVSRNSTVRYFNGTGVVQVQVHVLQGWEDKGSFTFOALHHDGRIVPAY 122
QY 219 KEIPMSVPEISSOHVPKTVGLSDAFMLNPSDPVPESSRSIFEVHRIELDPKSVTMSA 278
DB 123 KEIPVLVTQISSTNHPVKVGLSDAFVVRHRTQQIPNVRRRTIYEVHVELQMSKITNISA 182
QY 279 VEFTPLPTCLQHRSCDACMSSDLTFNCVCHVLRQCSSGDFRQYRQEWMDYCAQAEGRM 338
DB 183 VEMTPLPTCLQFNRGCGPCVSSQIGFNCVCHVLRQCSSGDFRQYRQEWMDYCAQAEGRM 242
QY 339 CEDFQDEHDSASPD--SFPYDGLTTS---SSLFIDSLTTEDDTKLPYAGDGLQ 393
DB 243 CENTPEVETSSRTTTTIGATTQFRVLTTRRAVTSQPTSLPTEDDTKIALHLKDNAS 302
QY 394 -NLSPKTKGTPVHLGTI 410
DB 303 TDDSAEKKGGTLLHAGLI 320

RESULT 12
US-09-181-706-2
; Sequence 2, Application US/09181706
; Patent No. 6130068
; GENERAL INFORMATION:
; APPLICANT: Melanie K. Spriggs, Michael R. Comeau,
; APPLICANT: Robert F. DuBoise, Richard S. Johnson
; TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
; TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janis C. Henry
; STREET: 51 University St.
; CITY: Seattle
; STATE: WA
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/181,706
; FILING DATE: October 28, 1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/958,598 (converted to a
; APPLICATION NUMBER: Provisional, see below)
; FILING DATE: October 28, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: --to be assigned-- (USN 08/958,598
; APPLICATION NUMBER: conversion to Provisional application)
; FILING DATE: October 26, 1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Henry, Janis C
; REGISTRATION NUMBER: 34,347
; REFERENCE/DOCKET NUMBER: 2631-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)470-4189
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1568 amino acids
```

```
;
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-181-706-2

Query Match          5.2%; Score 115.5; DB 3; Length 1568;
Best Local Similarity 20.6%; Pred. No. 0.074;
Matches 77; Conservative 42; Mismatches 118; Indels 137; Gaps 20;

Qy 22 GTVGRNRRARSPGHVSEPDRT-----QLSDLGSGTGLAMDTLPDNRTRVVEDNHNHYVS 77
Db 256 GAATGWPSMAR-----IAQSTEVLFGQASLDCGHG-----PDGR-----R 292
Qy 78 RLYGPSEPHSRELWVDV--AEANRSQVKIHTI-----LSNTHROASRVVLSF----- 122
Db 293 LLLSSSLVEALDVWAGVFAAGGQERRSPPTTALCLFRMSEIQARAKRVSWDFKTAES 352
Qy 123 -----DPPFYGHPLRQITATGGIFMGDVHRLMTATQYVAPLMANFNPYSDNSTVY 177
Db 353 HCKEGDQPERVQPIASSTL-----IHSDLTSV-YGTVM-----NRTVLF 391
Qy 178 PDNGTVFVQWDHYVLOGWEDKGSFTFOALHHDGRI--VFAYKEIPMSVPEI---SSSQ 232
Db 392 LGTG-----FYKLVPDP-----VKNIYIY-----DQLLKVLGENLTSNCEVIYEIKEE 422
Qy 233 HPVKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDFSKVTSMSAVEFTPLPTCLOHRS 292
Db 423 TPV-----FYKLVPDP-----VKNIYIY-----LTAGKEVRRIRVANCNKHKS 460
Qy 293 CDACMSDLTFNCWCHVLCSSGFDRYRQE-----WMDYCAQAEAGRMCEDFQ-----D 344
Db 461 CSECLTA-TDPHCGWCHSLQRTFGDCVHSENLENWLDI-----SSGAKKCPKIQRSS 515
Qy 345 EDHDSASPDTSFSP 358
Db 516 KEKTTVTWVGFSFP 529

RESULT 13
US-09-458-791-2
; Sequence 2, Application US/09458791
; Patent No. 6174689
; GENERAL INFORMATION:
; APPLICANT: Spriggs, Melanie
; TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
; RECEPTOR DNA AND POLYPEPTIDES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janis C. Henry
; STREET: 51 University St.
; CITY: Seattle
; STATE: WA
; COUNTRY: US
; ZIP: 98101
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS/Windows 95
; SOFTWARE: Word for Windows 95, 7.0a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/458,791
; FILING DATE: 10-Dec-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/958,598
; FILING DATE: 28-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Henry, Janis C
; REGISTRATION NUMBER: 34,347
; REFERENCE/DOCKET NUMBER: 2631
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)470-4189
; TELEFAX: (206)233-0644

;
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1569 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-458-791-2

Query Match          5.2%; Score 115.5; DB 3; Length 1568;
Best Local Similarity 20.6%; Pred. No. 0.074;
Matches 77; Conservative 42; Mismatches 118; Indels 137; Gaps 20;

Qy 22 GTVGRNRRARSPGHVSEPDRT-----QLSDLGSGTGLAMDTLPDNRTRVVEDNHNHYVS 77
Db 256 GAATGWPSMAR-----IAQSTEVLFGQASLDCGHG-----PDGR-----R 292
Qy 78 RLYGPSEPHSRELWVDV--AEANRSQVKIHTI-----LSNTHROASRVVLSF----- 122
Db 293 LLLSSSLVEALDVWAGVFAAGGQERRSPPTTALCLFRMSEIQARAKRVSWDFKTAES 352
Qy 123 -----DPPFYGHPLRQITATGGIFMGDVHRLMTATQYVAPLMANFNPYSDNSTVY 177
Db 353 HCKEGDQPERVQPIASSTL-----IHSDLTSV-YGTVM-----NRTVLF 391
Qy 178 PDNGTVFVQWDHYVLOGWEDKGSFTFOALHHDGRI--VFAYKEIPMSVPEI---SSSQ 232
Db 392 LGTG-----FYKLVPDP-----VKNIYIY-----DQLLKVLGENLTSNCEVIYEIKEE 422
Qy 233 HPVKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDFSKVTSMSAVEFTPLPTCLOHRS 292
Db 423 TPV-----FYKLVPDP-----VKNIYIY-----LTAGKEVRRIRVANCNKHKS 460
Qy 293 CDACMSDLTFNCWCHVLCSSGFDRYRQE-----WMDYCAQAEAGRMCEDFQ-----D 344
Db 461 CSECLTA-TDPHCGWCHSLQRTFGDCVHSENLENWLDI-----SSGAKKCPKIQRSS 515
Qy 345 EDHDSASPDTSFSP 358
Db 516 KEKTTVTWVGFSFP 529

RESULT 14
US-09-459-066-2
; Sequence 2, Application US/09459066
; Patent No. 6187909
; GENERAL INFORMATION:
; APPLICANT: Spriggs, Melanie
; TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
; RECEPTOR DNA AND POLYPEPTIDES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janis C. Henry
; STREET: 51 University St.
; CITY: Seattle
; STATE: WA
; COUNTRY: US
; ZIP: 98101
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS/Windows 95
; SOFTWARE: Word for Windows 95, 7.0a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/459,066
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/958,598
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Henry, Janis C
; REGISTRATION NUMBER: 34,347
```

REFERENCE/DOCKET NUMBER: 2631  
TELEPHONE: (206)470-4189  
TELEFAX: (206)233-0644  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1568 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-459-066-2

Query Match 5.2%; Score 115.5; DB 3; Length 1568;  
Best Local Similarity 20.6%; Pred. No. 0.074;  
Matches 77; Conservative 42; Mismatches 118; Indels 137; Gaps 20;  
Qy 22 GTVGRNRRARESPGHVSEPDRT-----QLSQDLGGGTLAMDTLPDNRTRVVEDNHSYVVS 77  
Db 256 GAATGWPSMAR-----IAQSTEVLFGQASLDCGHG-----PDGR-----R 292  
Qy 78 RLYGPSEPHSRELWVDV--AEANRSQVKIHTI-----LSNTHRQASRVVLSF----- 122  
Db 293 LLLSSSLVEALDVWAGVSAAGGQERRSPPTTALCLFRMSEIQARAKRVSWEFKTAES 352  
Qy 123 -----DPPFYGHPLRQITATGGFIFMGDVTHRMLTATQYVAPLMAFNPNPGYSDNSTVYV 177  
Db 353 HCKEGDQPERVQPIASSTL-----IHSDLTSV-YGTVM-----NRTVLF 391  
Qy 178 FDNGTVFVVDHVVYVLOGWEDKGSFTFOAALHHDGRI--VFAYKEIPMSVPEI---SSSQ 232  
Db 392 LGTG-----DQLLKVLIGENLTSNCPVIVEIKEE 422  
Qy 233 HPVKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDSPKVTSMASVEFTPLPTCLOHRS 292  
Db 423 TPV-----FYKLVPDP-----VKNIIY-----LTAGKEVRIRVANCNKHS 460  
Qy 293 CDACWSSDLTFCNSCHVLRQCSGFDYROR-----WMDYCAOAEGRMCEDFQ-----D 344  
Db 461 CSECLTA-TDPHCGWCHSLQRCFTQGCVCVHSENLENWLDI-----SSGAKKCPKIQRSS 515  
Qy 345 EDHDSASDTSFSP 358  
Db 516 KEKTTVTVMVGSFSP 529

RESULT 15

US-09-459-065-2  
Sequence 2, Application US/09459065  
Patent No. 6562949  
GENERAL INFORMATION:  
APPLICANT: Spriggs, Melanie  
TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN  
TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Janis C. Henry  
STREET: 51 University St.  
CITY: Seattle  
STATE: WA  
COUNTRY: US  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: MS-DOS/Windows 95  
SOFTWARE: Word for Windows 95, 7.0a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/459,065  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/958,598  
FILING DATE:

ATTORNEY/AGENT INFORMATION:  
NAME: Henry, Janis C  
REGISTRATION NUMBER: 34,347  
REFERENCE/DOCKET NUMBER: 2631  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)470-4189  
TELEFAX: (206)233-0644  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1568 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-459-065-2

Query Match 5.2%; Score 115.5; DB 4; Length 1568;  
Best Local Similarity 20.6%; Pred. No. 0.074;  
Matches 77; Conservative 42; Mismatches 118; Indels 137; Gaps 20;  
Qy 22 GTVGRNRRARESPGHVSEPDRT-----QLSQDLGGGTLAMDTLPDNRTRVVEDNHSYVVS 77  
Db 256 GAATGWPSMAR-----IAQSTEVLFGQASLDCGHG-----PDGR-----R 292  
Qy 78 RLYGPSEPHSRELWVDV--AEANRSQVKIHTI-----LSNTHRQASRVVLSF----- 122  
Db 293 LLLSSSLVEALDVWAGVSAAGGQERRSPPTTALCLFRMSEIQARAKRVSWEFKTAES 352  
Qy 123 -----DPPFYGHPLRQITATGGFIFMGDVTHRMLTATQYVAPLMAFNPNPGYSDNSTVYV 177  
Db 353 HCKEGDQPERVQPIASSTL-----IHSDLTSV-YGTVM-----NRTVLF 391  
Qy 178 FDNGTVFVVDHVVYVLOGWEDKGSFTFOAALHHDGRI--VFAYKEIPMSVPEI---SSSQ 232  
Db 392 LGTG-----DQLLKVLIGENLTSNCPVIVEIKEE 422  
Qy 233 HPVKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDSPKVTSMASVEFTPLPTCLOHRS 292  
Db 423 TPV-----FYKLVPDP-----VKNIIY-----LTAGKEVRIRVANCNKHS 460  
Qy 293 CDACWSSDLTFCNSCHVLRQCSGFDYROR-----WMDYCAOAEGRMCEDFQ-----D 344  
Db 461 CSECLTA-TDPHCGWCHSLQRCFTQGCVCVHSENLENWLDI-----SSGAKKCPKIQRSS 515  
Qy 345 EDHDSASDTSFSP 358  
Db 516 KEKTTVTVMVGSFSP 529

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Job time : 35.5649 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 28, 2005, 21:56:43 ; Search time 5.28163 Seconds  
(without alignments)  
816.164 Million cell updates/sec

Title: US-09-918-715-230\_COPY\_280\_344  
Perfect score: 370  
Sequence: 1 YHRIELPSKVTSMASVEFT.....CHVLQRCSSGFDYRQEWMD 65

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents\_AA.\*

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- 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pdp.\*
- 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pdp.\*
- 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pdp.\*
- 5: /cgn2\_6/ptodata/1/iaa/PTUS\_COMB.pdp.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles.pdp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	359	97.0	431	4	US-09-912-935-36
2	264	71.4	530	4	US-09-912-935-38
3	263	71.1	392	4	US-09-764-325A-23
4	263	71.1	392	4	US-09-764-325A-25
5	263	71.1	392	4	US-09-912-935-23
6	263	71.1	392	4	US-09-912-935-25
7	263	71.1	425	4	US-09-912-935-35
8	263	71.1	449	4	US-09-912-935-34
9	263	71.1	499	4	US-09-912-935-31
10	263	71.1	529	4	US-09-912-935-28
11	263	71.1	529	4	US-09-912-935-40
12	101	27.3	1568	3	US-09-181-706-2
13	101	27.3	1568	3	US-09-458-791-2
14	101	27.3	1568	3	US-09-459-086-2
15	101	27.3	1568	4	US-09-459-065-2
16	63.5	17.2	846	2	US-07-728-215-33
17	63.5	17.2	846	3	US-08-938-085A-33
18	63.5	17.2	846	4	US-10-072-844-33
19	63.5	17.2	846	4	US-10-072-838-33
20	63.5	17.2	846	4	US-10-072-841A-33
21	63.5	17.2	846	4	US-10-219-631-33
22	63	17.0	1404	4	US-09-345-473E-24
23	62.5	16.9	871	3	US-09-245-041-19
24	62.5	16.9	871	4	US-09-358-055B-19
25	62.5	16.9	871	4	US-09-893-238-19
26	62.5	16.9	1198	3	US-09-245-041-131
27	62.5	16.9	1198	3	US-09-794-236-3

28	62.5	16.9	1198	4	US-09-358-055B-132	Sequence 132, App
29	62.5	16.9	1350	3	US-09-245-041-17	Sequence 17, Appl
30	62.5	16.9	1350	4	US-09-358-055B-17	Sequence 17, Appl
31	62.5	16.9	1350	4	US-09-893-238-17	Sequence 17, Appl
32	62.5	16.9	1429	3	US-09-245-041-130	Sequence 130, App
33	62.5	16.9	1429	4	US-09-358-055B-131	Sequence 131, App
34	62.5	16.9	2787	3	US-09-245-041-15	Sequence 15, Appl
35	62.5	16.9	2787	4	US-09-358-055B-15	Sequence 15, Appl
36	62.5	16.9	2787	4	US-09-893-238-15	Sequence 15, Appl
37	61	16.5	138	4	US-09-898-659-30	Sequence 30, Appl
38	60.5	16.4	121	4	US-09-270-767-38436	Sequence 38436, A
39	60.5	16.4	121	4	US-09-270-767-38436	Sequence 38436, A
40	60	16.2	704	4	US-09-370-838-191	Sequence 191, App
41	60	16.2	704	4	US-09-854-133-191	Sequence 191, App
42	59.5	16.1	59	4	US-09-513-999C-6708	Sequence 6708, Ap
43	59.5	16.1	363	4	US-09-252-991A-17517	Sequence 17517, A
44	59.5	16.1	939	4	US-09-854-845-16	Sequence 16, Appl
45	59.5	16.1	954	4	US-09-854-845-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1  
US-09-912-935-36  
; Sequence 36, Application US/09912935  
; Patent No. 6673904  
; GENERAL INFORMATION:  
; APPLICANT: Nishikawa, Mitsuo et al.  
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE  
; FILE REFERENCE: 32066/37483  
; CURRENT APPLICATION NUMBER: US/09/912.935  
; CURRENT FILING DATE: 2001-07-24  
; PRIOR APPLICATION NUMBER: PCT/US00/35260  
; PRIOR FILING DATE: 2000-12-23  
; NUMBER OF SEQ ID NOS: 53  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 36  
; LENGTH: 431  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-912-935-36

Query Match 97.0%; Score 359; DB 4; Length 431;  
Best Local Similarity 100.0%; Pred.No. 1.5e-36;  
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	YHRIELPSKVTSMASVEFTPLPTCLQHRSCDACMSSDLTFNCNCHVLQRCSSGFDYR 60
Db	209	YHRIELPSKVTSMASVEFTPLPTCLQHRSCDACMSSDLTFNCNCHVLQRCSSGFDYR 268
Qy	61	QEW 63
Db	269	QEW 271

RESULT 2  
US-09-912-935-38  
; Sequence 38, Application US/09912935  
; Patent No. 6673904  
; GENERAL INFORMATION:  
; APPLICANT: Nishikawa, Mitsuo et al.  
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE  
; FILE REFERENCE: 32066/37483  
; CURRENT APPLICATION NUMBER: US/09/912.935  
; CURRENT FILING DATE: 2001-07-24  
; PRIOR APPLICATION NUMBER: PCT/US00/35260  
; PRIOR FILING DATE: 2000-12-23  
; NUMBER OF SEQ ID NOS: 53  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 38



FILE REFERENCE: 32066/37483  
CURRENT APPLICATION NUMBER: US/09/912,935  
CURRENT FILING DATE: 2001-07-24  
PRIOR APPLICATION NUMBER: PCT/US00/35260  
PRIOR FILING DATE: 2000-12-23  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 25  
LENGTH: 392  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-912-935-25

Query Match 71.1%; Score 263; DB 4; Length 392;  
Best Local Similarity 67.7%; Pred. No. 1.1e-24;  
Matches 44; Conservative 9; Mismatches 12; Indels 0; Gaps 0;  
Qy 1 YHRIELDPKVTSMASAVEFTPLPTCLOHRSCDACMSSDLTENCSCWCHVLCRCSSGFDYR 60  
Db 167 YHVELQMSKITNISAVEMTLPCTCLOFNRCGPCVSSQIGFNCWSCSKLQRCSSGFDHR 226  
Qy 61 QEWMD 65  
Db 227 QDWVD 231

RESULT 7  
US-09-912-935-35  
Sequence 35, Application US/09912935  
Patent No. 6673904  
GENERAL INFORMATION:  
APPLICANT: Nishikawa, Mitsuo et al.  
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE  
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES  
FILE REFERENCE: 32066/37483  
CURRENT APPLICATION NUMBER: US/09/912,935  
CURRENT FILING DATE: 2001-07-24  
PRIOR APPLICATION NUMBER: PCT/US00/35260  
PRIOR FILING DATE: 2000-12-23  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 35  
LENGTH: 425  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-912-935-35

Query Match 71.1%; Score 263; DB 4; Length 425;  
Best Local Similarity 67.7%; Pred. No. 1.3e-24;  
Matches 44; Conservative 9; Mismatches 12; Indels 0; Gaps 0;  
Qy 1 YHRIELDPKVTSMASAVEFTPLPTCLOHRSCDACMSSDLTENCSCWCHVLCRCSSGFDYR 60  
Db 202 YHVELQMSKITNISAVEMTLPCTCLOFNRCGPCVSSQIGFNCWSCSKLQRCSSGFDHR 261  
Qy 61 QEWMD 65  
Db 262 QDWVD 266

RESULT 8  
US-09-912-935-34  
Sequence 34, Application US/09912935  
Patent No. 6673904  
GENERAL INFORMATION:  
APPLICANT: Nishikawa, Mitsuo et al.  
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE  
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES  
FILE REFERENCE: 32066/37483  
CURRENT APPLICATION NUMBER: US/09/912,935  
CURRENT FILING DATE: 2001-07-24  
PRIOR APPLICATION NUMBER: PCT/US00/35260  
PRIOR FILING DATE: 2000-12-23

NUMBER OF SEQ ID NOS: 53  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 34  
LENGTH: 449  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-912-935-34

Query Match 71.1%; Score 263; DB 4; Length 449;  
Best Local Similarity 67.7%; Pred. No. 1.3e-24;  
Matches 44; Conservative 9; Mismatches 12; Indels 0; Gaps 0;  
Qy 1 YHRIELDPKVTSMASAVEFTPLPTCLOHRSCDACMSSDLTENCSCWCHVLCRCSSGFDYR 60  
Db 304 YHVELQMSKITNISAVEMTLPCTCLOFNRCGPCVSSQIGFNCWSCSKLQRCSSGFDHR 363  
Qy 61 QEWMD 65  
Db 364 QDWVD 368

RESULT 9  
US-09-912-935-31  
Sequence 31, Application US/09912935  
Patent No. 6673904  
GENERAL INFORMATION:  
APPLICANT: Nishikawa, Mitsuo et al.  
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE  
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES  
FILE REFERENCE: 32066/37483  
CURRENT APPLICATION NUMBER: US/09/912,935  
CURRENT FILING DATE: 2001-07-24  
PRIOR APPLICATION NUMBER: PCT/US00/35260  
PRIOR FILING DATE: 2000-12-23  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 31  
LENGTH: 499  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-912-935-31

Query Match 71.1%; Score 263; DB 4; Length 499;  
Best Local Similarity 67.7%; Pred. No. 1.5e-24;  
Matches 44; Conservative 9; Mismatches 12; Indels 0; Gaps 0;  
Qy 1 YHRIELDPKVTSMASAVEFTPLPTCLOHRSCDACMSSDLTENCSCWCHVLCRCSSGFDYR 60  
Db 274 YHVELQMSKITNISAVEMTLPCTCLOFNRCGPCVSSQIGFNCWSCSKLQRCSSGFDHR 333  
Qy 61 QEWMD 65  
Db 334 QDWVD 338

RESULT 10  
US-09-912-935-28  
Sequence 28, Application US/09912935  
Patent No. 6673904  
GENERAL INFORMATION:  
APPLICANT: Nishikawa, Mitsuo et al.  
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE  
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES  
FILE REFERENCE: 32066/37483  
CURRENT APPLICATION NUMBER: US/09/912,935  
CURRENT FILING DATE: 2001-07-24  
PRIOR APPLICATION NUMBER: PCT/US00/35260  
PRIOR FILING DATE: 2000-12-23  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 28  
LENGTH: 529  
TYPE: PRT





```

;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)470-4189
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1568 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-458-791-2

Query Match 27.3%; Score 101; DB 3; Length 1568;
Best Local Similarity 29.7%; Pred. No. 0.00079;
Matches 22; Conservative 15; Mismatches 27; Indels 10; Gaps 3;

Qy 1 YHRIELDPK-----VTSMASAVEFTPLPTCLQHRSCDACMSSDLTFNCSCWCHVLQRCSSG 55
Db 426 FYKLVPDPVKNIYIYLTAGKEVRRIRVANCNKHKSCSECLTA-TDPHCGWCHSLQRCFTQ 484
Qy 56 FDRYRQE-----WMD 65
Db 485 GDCVHSENLENWLD 498

RESULT 14
US-09-459-066-2
; Sequence 2, Application US/09459066
; Patent No. 6187909
; GENERAL INFORMATION:
; APPLICANT: Spriggs, Melanie
; TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janis C. Henry
; STREET: 51 University St.
; CITY: Seattle
; STATE: WA
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS/Windows 95
; SOFTWARE: Word for Windows 95, 7.0a
; CURRENT APPLICATION DATA: US/09/459,066
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/958,598
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Henry, Janis C
; REGISTRATION NUMBER: 34,347
; REFERENCE/DOCKET NUMBER: 2631
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)470-4189
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1568 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-459-065-2

Query Match 27.3%; Score 101; DB 4; Length 1568;
Best Local Similarity 29.7%; Pred. No. 0.00079;
Matches 22; Conservative 15; Mismatches 27; Indels 10; Gaps 3;

Qy 1 YHRIELDPK-----VTSMASAVEFTPLPTCLQHRSCDACMSSDLTFNCSCWCHVLQRCSSG 55
Db 426 FYKLVPDPVKNIYIYLTAGKEVRRIRVANCNKHKSCSECLTA-TDPHCGWCHSLQRCFTQ 484
Qy 56 FDRYRQE-----WMD 65
Db 485 GDCVHSENLENWLD 498

Search completed: January 28, 2005, 22:14:14
Job time : 6.53163 secs
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;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)470-4189
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1568 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-458-791-2

Query Match 27.3%; Score 101; DB 3; Length 1568;
Best Local Similarity 29.7%; Pred. No. 0.00079;
Matches 22; Conservative 15; Mismatches 27; Indels 10; Gaps 3;

Qy 1 YHRIELDPK-----VTSMASAVEFTPLPTCLQHRSCDACMSSDLTFNCSCWCHVLQRCSSG 55
Db 426 FYKLVPDPVKNIYIYLTAGKEVRRIRVANCNKHKSCSECLTA-TDPHCGWCHSLQRCFTQ 484
Qy 56 FDRYRQE-----WMD 65
Db 485 GDCVHSENLENWLD 498

RESULT 14
US-09-459-066-2
; Sequence 2, Application US/09459066
; Patent No. 6187909
; GENERAL INFORMATION:
; APPLICANT: Spriggs, Melanie
; TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janis C. Henry
; STREET: 51 University St.
; CITY: Seattle
; STATE: WA
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS/Windows 95
; SOFTWARE: Word for Windows 95, 7.0a
; CURRENT APPLICATION DATA: US/09/459,066
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/958,598
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Henry, Janis C
; REGISTRATION NUMBER: 34,347
; REFERENCE/DOCKET NUMBER: 2631
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)470-4189
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1568 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-459-066-2

Query Match 27.3%; Score 101; DB 3; Length 1568;
Best Local Similarity 29.7%; Pred. No. 0.00079;
Matches 22; Conservative 15; Mismatches 27; Indels 10; Gaps 3;

Qy 1 YHRIELDPK-----VTSMASAVEFTPLPTCLQHRSCDACMSSDLTFNCSCWCHVLQRCSSG 55
Db 426 FYKLVPDPVKNIYIYLTAGKEVRRIRVANCNKHKSCSECLTA-TDPHCGWCHSLQRCFTQ 484
Qy 56 FDRYRQE-----WMD 65
Db 485 GDCVHSENLENWLD 498

Search completed: January 28, 2005, 22:14:14
Job time : 6.53163 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 28, 2005, 21:52:02 ; Search time 130.231 Seconds  
(without alignments)  
1129.372 Million cell updates/sec

Title: US-09-918-715-230\_COPY\_18\_427

Perfect score: 2218  
Sequence: 1 ALSFPQAGHDEFGSGWAA.....GLQNNLSPTKGFVHLGTI 410

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Geneseq\_23Sep04:.\*  
1: Geneseqp1980s:.\*  
2: Geneseqp1990s:.\*  
3: Geneseqp2000s:.\*  
4: Geneseqp2001s:.\*  
5: Geneseqp2002s:.\*  
6: Geneseqp2003as:.\*  
7: Geneseqp2003bs:.\*  
8: Geneseqp2004s:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2218	100.0	500	5	ABB90749 Human Tum
2	2218	100.0	500	6	ABU54456 Human tum
3	2218	100.0	500	7	ADI21063 Novel hum
4	2218	100.0	500	8	ADH13230 Human mal
5	2218	100.0	527	7	ADI21554 Novel hum
6	2218	100.0	527	7	ADI21553 Novel hum
7	2218	100.0	1002	5	ABB90723 Human Tum
8	2218	100.0	1002	6	ABU54430 Human tum
9	2134	96.2	488	7	ADI21064 Novel hum
10	1924	86.7	400	3	AAB43131 Human ORF
11	1799.5	81.1	500	5	ABB90783 Mouse Tum
12	1799.5	81.1	500	5	ABB90729 Mouse Tum
13	1799.5	81.1	500	6	ABU54436 Mouse tum
14	1799.5	81.1	500	6	ABU54490 Mouse tum
15	1795	80.9	431	4	AAB85400 Tumour en
16	1795	80.9	431	6	ABO01434 Human tum
17	1215	54.8	240	7	ADB65558 Human pro
18	1066.5	48.1	486	4	AAM39067 Human pol
19	1066.5	48.1	499	4	AAB85396 Stem cell
20	1066.5	48.1	499	6	ABO01430 Human ste
21	1066.5	48.1	529	4	AAB31211 Amino aci
22	1066.5	48.1	529	4	AAB85394 Stem cell
23	1066.5	48.1	529	4	AAU29259 Human PRO
24	1066.5	48.1	529	4	AAM39068 Human pol
25	1066.5	48.1	529	5	ABB90734 Human Tum

26	1066.5	48.1	529	5	ABB90726	Abb90726 Human Tum
27	1066.5	48.1	529	5	ABP53349	ABp53349 Human tra
28	1066.5	48.1	529	5	ABG69157	ABg69157 Human ste
29	1066.5	48.1	529	5	ABG69161	ABg69161 Human pro
30	1066.5	48.1	529	5	ABU58635	ABu58635 Human PRO
31	1066.5	48.1	529	6	ABU88183	ABu88183 Novel hum
32	1066.5	48.1	529	6	ABU84498	ABu84498 Human sec
33	1066.5	48.1	529	6	ABR66372	ABr66372 Human sec
34	1066.5	48.1	529	6	ABR65762	ABr65762 Human sec
35	1066.5	48.1	529	6	ABU99702	ABu99702 Human sec
36	1066.5	48.1	529	6	ABU82941	ABu82941 Human PRO
37	1066.5	48.1	529	6	ABU90062	ABu90062 Novel hum
38	1066.5	48.1	529	6	ABR68311	ABr68311 Human sec
39	1066.5	48.1	529	6	ABU96364	ABu96364 Novel hum
40	1066.5	48.1	529	6	ABU92795	ABu92795 Human sec
41	1066.5	48.1	529	6	ABO08872	ABo08872 Human sec
42	1066.5	48.1	529	6	ABO02924	ABo02924 Human sec
43	1066.5	48.1	529	6	ABR75078	ABr75078 Human sec
44	1066.5	48.1	529	6	ABR94840	ABr94840 Human sec
45	1066.5	48.1	529	6	ABO25182	ABo25182 Novel hum

ALIGNMENTS

RESULT 1  
ABB90749  
ID ABB90749 standard; protein; 500 AA.  
XX  
AC ABB90749;  
XX  
DT 30-MAY-2002 (first entry)  
XX  
DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 230.  
XX  
KW Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic;  
KW normal endothelial marker; pan-endothelial marker; immunostimulant;  
KW antiangiogenic; tumour; neoangiogenesis; vascularised tumour;  
KW polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;  
KW psoriasis.  
XX  
OS Homo sapiens.  
XX  
FN WO200210217-A2.  
XX  
PD 07-FEB-2002.  
XX  
PF 01-AUG-2001; 2001WO-US024031.  
XX  
PR 02-AUG-2000; 2000US-0222599P.  
PR 11-AUG-2000; 2000US-0224360P.  
PR 11-APR-2001; 2001US-0282850P.  
PA (UYJO ) UNIV JOHNS HOPKINS.  
XX  
PI St Croix B, Kinzler KW, Vogelstein B;  
XX  
DR WPI; 2002-291856/33.  
XX  
DR N-PSDB; ABL92103.  
XX  
PT An isolated molecule comprising an antibody variable region which  
PT specifically binds to an extracellular domain of a tumor endothelial  
PT marker (TEM) protein, useful for inhibiting tumor growth.  
XX  
XX  
PS Claim 1; Page 206-207; 331pp; English.  
XX  
CC The invention relates to an isolated molecule comprising an antibody  
CC variable region which specifically binds to an extracellular domain of a  
CC tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740,  
CC ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM  
CC proteins have cytostatic, immunostimulant and antiangiogenic activity.  
CC They are useful for inhibiting tumour growth, neoangiogenesis in subjects  
CC bearing a vascularised tumour, polycystic kidney disease, diabetic

CC retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM  
CC genes and the encoded proteins (ABL92075-ABL92141 and ABB90721-ABB90789)  
CC are disclosed, as are marker oligonucleotide sequences: tumour  
CC endothelial markers (TEM) ABL9196-ABL92041 and ABL92143-ABL92191; normal  
CC endothelial markers (NEM) ABL92042-ABL92074; and pan-endothelial markers  
CC (PEM) ABL91903-ABL91995  
XX  
SQ Sequence 500 AA;

Query Match 100.0%; Score 2218; DB 5; Length 500;  
Best Local Similarity 100.0%; Pred. No. 2.7e-211;  
Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ALSPPQAGHDEGPGSGWAAKGTVRGWNRRARESPGHVSEPDRTQLSDLGGGTLAMDTL 60  
Db |||||  
Qy 18 ALSPPQAGHDEGPGSGWAAKGTVRGWNRRARESPGHVSEPDRTQLSDLGGGTLAMDTL 77  
Db |||||  
Qy 61 PDNRTRVVEDNHSYVSRLYGPPSPHRELVDAEAEANRSQVKIHTILSNTHROASRVVL 120  
Db |||||  
Qy 78 PDNRTRVVEDNHSYVSRLYGPPSPHRELVDAEAEANRSQVKIHTILSNTHROASRVVL 137  
Db |||||  
Qy 121 SFDPFFYGHPLRQITATGGIFMGDVVHRMLTATQVAPLMANFNPGYSDNSTVVFYFDN 180  
Db |||||  
Qy 138 SFDPFFYGHPLRQITATGGIFMGDVVHRMLTATQVAPLMANFNPGYSDNSTVVFYFDN 197  
Db |||||  
Qy 181 GTVFVQWHDVYLOGWEDKGSFTFQAAALHHDGRIVFAKPEIPMSVPEISSQHPVKTGLS 240  
Db |||||  
Qy 198 GTVFVQWHDVYLOGWEDKGSFTFQAAALHHDGRIVFAKPEIPMSVPEISSQHPVKTGLS 257  
Db |||||  
Qy 241 DAFMILNPSDPVPESRRRSIFEYHRIELDPKVTSMASAVEFTPLPTCLOHRSACDACMSD 300  
Db |||||  
Qy 258 DAFMILNPSDPVPESRRRSIFEYHRIELDPKVTSMASAVEFTPLPTCLOHRSACDACMSD 317  
Db |||||  
Qy 301 LTFNCNCHVLRQCSGFDRIYQWMDYGCQAQAEGRMCEDFQDEHDSASPDTSFSPYD 360  
Db |||||  
Qy 318 LTFNCNCHVLRQCSGFDRIYQWMDYGCQAQAEGRMCEDFQDEHDSASPDTSFSPYD 377  
Db |||||  
Qy 361 GDLTTSSSLFIDSLTTEDDTKLNYPAGGDLQNNLSPKTKGTPVHLGTI 410  
Db 378 GDLTTSSSLFIDSLTTEDDTKLNYPAGGDLQNNLSPKTKGTPVHLGTI 427

RESULT 2  
ABU54456  
ID ABU54456 standard; protein; 500 AA.

XX AC ABU54456;

XX DT 12-MAR-2003 (first entry)

XX DE Human tumour endothelial marker TEM 17.

XX Human; endothelial cell; EC; tumour endothelial cell; TEM; NEM;  
KW Tumour endothelial marker; normal endothelial marker; PEM;  
KW pan-endothelial marker; polycystic kidney disease; psoriasis;  
KW diabetic retinopathy; rheumatoid arthritis; tumour angiogenesis;  
KW neovascularization; immune response; cytostatic; antidiabetic;  
KW ophthalmological; antirheumatic; antiarthritic; antipsoriatic.

XX OS Homo sapiens.

XX PN WO200283874-A2.

XX PD 24-OCT-2002.

XX XX 10-APR-2002; 2002WO-0080253.

XX XX 11-APR-2001; 2001US-0282850P.

XX PR 06-FEB-2002; 2002US-0354262P.

XX XX (UTJO ) UNIV JOHNS HOPKINS.

XX FA Carson-Walter E, St Croix B, Kinzler KW, Vogelstein B;

XX PI

XX  
DR  
XX  
XX  
PT  
PT  
PT  
XX  
PS  
XX  
CC  
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CC  
CC  
SQ

WPI: 2003-093016/08.  
N-PSDB; ABX72028.

New purified human transmembrane protein, designated as tumor endothelial marker (TEM) 3, useful for detecting, diagnosing or treating tumors, polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis or psoriasis.

Disclosure; Page 221-222; 374pp; English.

The present invention relates to a novel method for the isolation of endothelial cells (ECs), and the identification of genes expressed in normal and tumour ECs. Tumour endothelial marker (TEM), normal endothelial marker (NEM), and pan-endothelial marker (PEM) genes are identified in human ECs. The human EC marker proteins and the polynucleotide sequences encoding them are useful for detecting, diagnosing or treating tumours as well as polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are also useful for inhibiting neovascularization or tumour angiogenesis, for inducing an immune response to tumour endothelial cells in a patient, or for identifying candidate drugs for treating tumours. The present sequence represents a human TEM or NEM protein of the invention

Sequence 500 AA;

Query Match 100.0%; Score 2218; DB 6; Length 500;  
Best Local Similarity 100.0%; Pred. No. 2.7e-211;  
Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALSPPQAGHDEGPGSGWAAKGTVRGWNRRARESPGHVSEPDRTQLSDLGGGTLAMDTL 60

Db 18 ALSPPQAGHDEGPGSGWAAKGTVRGWNRRARESPGHVSEPDRTQLSDLGGGTLAMDTL 77

Qy 61 PDNRTRVVEDNHSYVSRLYGPPSPHRELVDAEAEANRSQVKIHTILSNTHROASRVVL 120

Db 78 PDNRTRVVEDNHSYVSRLYGPPSPHRELVDAEAEANRSQVKIHTILSNTHROASRVVL 137

Qy 121 SFDPFFYGHPLRQITATGGIFMGDVVHRMLTATQVAPLMANFNPGYSDNSTVVFYFDN 180

Db 138 SFDPFFYGHPLRQITATGGIFMGDVVHRMLTATQVAPLMANFNPGYSDNSTVVFYFDN 197

Qy 181 GTVFVQWHDVYLOGWEDKGSFTFQAAALHHDGRIVFAKPEIPMSVPEISSQHPVKTGLS 240

Db 198 GTVFVQWHDVYLOGWEDKGSFTFQAAALHHDGRIVFAKPEIPMSVPEISSQHPVKTGLS 257

Qy 241 DAFMILNPSDPVPESRRRSIFEYHRIELDPKVTSMASAVEFTPLPTCLOHRSACDACMSD 300

Db 258 DAFMILNPSDPVPESRRRSIFEYHRIELDPKVTSMASAVEFTPLPTCLOHRSACDACMSD 317

Qy 301 LTFNCNCHVLRQCSGFDRIYQWMDYGCQAQAEGRMCEDFQDEHDSASPDTSFSPYD 360

Db 318 LTFNCNCHVLRQCSGFDRIYQWMDYGCQAQAEGRMCEDFQDEHDSASPDTSFSPYD 377

Qy 361 GDLTTSSSLFIDSLTTEDDTKLNYPAGGDLQNNLSPKTKGTPVHLGTI 410

Db 378 GDLTTSSSLFIDSLTTEDDTKLNYPAGGDLQNNLSPKTKGTPVHLGTI 427

RESULT 3

ADI21063

ID ADI21063 standard; protein; 500 AA.

XX AC ADI21063;

XX DT 15-APR-2004 (first entry)

XX DE Novel human protein #38.

XX forensic; nutritional source; damaged tissue; diseased tissue;  
KW myeloid cell disorder; lymphoid cell disorder;  
KW bone cartilage tissue growth; tendon tissue growth;  
KW ligament tissue growth; nerve tissue growth; regeneration; wound healing;

KW tissue repair; tissue replacement; burn; incision; ulcer; cancer; human.  
XX Homo sapiens.  
XX WO2003025148-A2.  
XX 27-MAR-2003.  
XX 19-SEP-2002; 2002WO-US029964.  
XX 19-SEP-2001; 2001US-0323739P.  
XX 13-SEP-2002; 2002US-0023739.  
XX (HYSE-) HYSEQ INC.  
XX Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao Qa, Wang J;  
XX Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang D;  
XX Haley-Vicente D;  
XX WPI; 2003-354603/33.  
XX N-PSDB; ADI21779.  
XX New polynucleotides and secreted proteins, useful for treating myeloid or  
XX lymphoid cell disorders, in bone cartilage, tendon, ligament and nerve  
XX tissue growth or regeneration, in wound healing, and in tissue repair and  
XX replacement.  
XX Claim 20; SEQ ID NO 314; 156pp; English.  
XX The invention relates to an isolated polynucleotide encoding a  
XX polypeptide with biological activity. The polynucleotides and  
XX polypeptides are useful in diagnostics, forensics, gene mapping,  
XX identification of mutations responsible for genetic disorders and other  
XX traits, to assess biodiversity, as nutritional sources or supplements.  
XX The polynucleotides may also be used as molecular weight markers,  
XX chromosome markers or map related gene positions, or as an antigen to  
XX raise anti-DNA antibodies or elicit immune response. The polypeptides are  
XX useful for raising antibodies, as markers for tissues in which the  
XX corresponding polypeptide is expressed, for re-engineering damaged or  
XX diseased tissues, for treating myeloid or lymphoid cell disorders, in  
XX bone cartilage, tendon, ligament and/or nerve tissue growth or  
XX regeneration, in wound healing, in tissue repair and replacement, in  
XX healing of burns, incisions and ulcers, and in treating cancer. The  
XX present sequence represents the amino acid sequence of a novel human  
XX protein.  
XX Sequence 500 AA;  
Query Match 100.0%; Score 2218; DB 7; Length 500;  
Best Local Similarity 100.0%; Pred. No. 2.7e-211;  
Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ALSPPQAGHDEPGSGWAAKGTVRGNRRRARESPGHVSEPDRTQLSQDLGGGTAMDTL 60  
DB 18 ALSPPQAGHDEPGSGWAAKGTVRGNRRRARESPGHVSEPDRTQLSQDLGGGTAMDTL 77  
QY 61 PDNRTRVVDNHSYVSRLYGSPSPHRSRLWVDVAEARNRSQVKTHTLSNTHRSQSRVL 120  
DB 78 PDNRTRVVDNHSYVSRLYGSPSPHRSRLWVDVAEARNRSQVKTHTLSNTHRSQSRVL 137  
QY 121 SFDPPFPYGHPLRQITTIATGPFIFMGDVIHRMLTATQYVAPLMANFPGYSDNSTVYFDN 180  
DB 138 SFDPPFPYGHPLRQITTIATGPFIFMGDVIHRMLTATQYVAPLMANFPGYSDNSTVYFDN 197  
QY 181 GTVPVQWDHYVLOGWEDKSGFTFOAALHDGRIVPAYKIPMSVPEISSQHPVKTGLS 240  
DB 198 GTVPVQWDHYVLOGWEDKSGFTFOAALHDGRIVPAYKIPMSVPEISSQHPVKTGLS 257  
QY 241 DAFMLNPSDVPESRRRSIFEYHRIELDPKSTMSGAVFTPLPTCLQRSCDACMSSD 300  
DB 258 DAFMLNPSDVPESRRRSIFEYHRIELDPKSTMSGAVFTPLPTCLQRSCDACMSSD 317  
QY 301 LTFNCSCWHLQRCSSGFDYRQEMWDYGCQAEGRMCEDFQDEHDSASPTSFSPYD 360

DB 318 LTFNCSCWHLQRCSSGFDYRQEMWDYGCQAEGRMCEDFQDEHDSASPTSFSPYD 377  
QY 361 GDLTTTSSSLFIDSLTTEDDTKLNYPAGGDLQNNLSPKTKGTPVHLGTI 410  
DB 378 GDLTTTSSSLFIDSLTTEDDTKLNYPAGGDLQNNLSPKTKGTPVHLGTI 427  
RESULT 4  
ADHI3230  
ID ADHI3230 standard; protein; 500 AA.  
XX ADHI3230;  
XX 11-MAR-2004 (first entry)  
XX Human malignant neoplasia-related protein SeqID79.  
XX malignant neoplasia; cytostatic; breast cancer; ovarian cancer;  
XX gastric cancer; colon cancer; oesophageal cancer; mesenchymal cancer;  
XX bladder cancer; non-small cell lung cancer; human.  
XX Homo sapiens.  
XX EP1365034-A2.  
XX 26-NOV-2003.  
XX 09-MAY-2003; 2003EP-00010447.  
XX 21-MAY-2002; 2002EP-00010291.  
XX 13-FEB-2003; 2003EP-00003112.  
XX (FARB ) BAYER AG.  
XX Wirtz R, Munnes M, Kallabis H;  
XX WPI; 2004-073279/08.  
XX N-PSDB; ADHI3207.  
XX Predicting, diagnosing or prognosing malignant neoplasia by detecting at  
XX least two markers, where the markers are genes from one or more  
XX chromosomal regions altered in malignant neoplasia,.  
XX Claim 11; SEQ ID NO 79; 267pp; English.  
XX This invention relates to a novel method for the prediction, diagnosis,  
XX or prognosis of malignant neoplasia by the detection of at least two  
XX markers. The invention may also be useful for the development of  
XX cytostatic compounds through the regulation of the expression of a gene  
XX or activity of a protein associated with malignant neoplasia. The method  
XX is useful for prediction, diagnosis or prognosis of malignant neoplasia  
XX such as breast cancer, ovarian cancer, gastric cancer, colon cancer,  
XX oesophageal cancer, mesenchymal cancer, bladder cancer or non-small cell  
XX lung cancer. The polynucleotides and polypeptides defined in the  
XX specification, antisense polynucleotides targeting the polynucleotides,  
XX antibodies targeting either one of the polynucleotides or polypeptides,  
XX and compounds identified by the screening methods are useful for  
XX preventing or treating malignant neoplasia. The disease treated is  
XX preferably breast cancer. The present sequence is that of a human  
XX the invention.  
XX Sequence 500 AA;  
Query Match 100.0%; Score 2218; DB 8; Length 500;  
Best Local Similarity 100.0%; Pred. No. 2.7e-211;  
Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ALSPPQAGHDEPGSGWAAKGTVRGNRRRARESPGHVSEPDRTQLSQDLGGGTAMDTL 60  
DB 18 ALSPPQAGHDEPGSGWAAKGTVRGNRRRARESPGHVSEPDRTQLSQDLGGGTAMDTL 77

QY 61 PDNRTRVVDNHSYVSRLYGSPSEPHSRELVDAEANRSQVKIHTILSNTHROASRVVL 120  
DB 78 PDNRTRVVDNHSYVSRLYGSPSEPHSRELVDAEANRSQVKIHTILSNTHROASRVVL 137  
QY 121 SFDPFFYGHPLRQITTIATGGFIHMDVTHRLMTATQYVAPLMAFNFGYSDNSTVYVFDN 180  
DB 138 SFDPFFYGHPLRQITTIATGGFIHMDVTHRLMTATQYVAPLMAFNFGYSDNSTVYVFDN 197  
QY 181 GTVFVQWDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHPVKTGLS 240  
DB 198 GTVFVQWDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHPVKTGLS 257  
QY 241 DAFMLNPSDPVPESRRRSIFEYHRIELDPKVTSMGSAVEFTPLPTCLOHRSCDACMSSD 300  
DB 258 DAFMLNPSDPVPESRRRSIFEYHRIELDPKVTSMGSAVEFTPLPTCLOHRSCDACMSSD 317  
QY 301 LTFNCSCWHLQRCSSGFDYRQEWMDYGCQAEGRMCEDFQDEHDSASPDTSFSPYD 360  
DB 318 LTFNCSCWHLQRCSSGFDYRQEWMDYGCQAEGRMCEDFQDEHDSASPDTSFSPYD 377  
QY 361 GDLTTSSSLFIDSLTTEDDTKLNPNYAGDGLQNNLSPKTKGTPVHLGTI 410  
DB 378 GDLTTSSSLFIDSLTTEDDTKLNPNYAGDGLQNNLSPKTKGTPVHLGTI 427

RESULT 5

ID ADI21554 standard; protein; 527 AA.  
XX AC ADI21554;  
DT 15-APR-2004 (first entry)  
XX DE Novel human polypeptide #33.  
XX KW forensic; nutritional source; damaged tissue; diseased tissue;  
KW myeloid cell disorder; lymphoid cell disorder;  
KW bone cartilage tissue growth; tendon tissue growth;  
KW ligament tissue growth; nerve tissue growth; regeneration; wound healing;  
KW tissue repair; tissue replacement; burn; incision; ulcer; cancer; human.  
XX OS Homo sapiens.  
XX PN WO2003025148-A2.  
XX PD 27-MAR-2003.  
XX PF 19-SEP-2002; 2002WO-US029964.  
XX PR 19-SEP-2001; 2001US-0323739P.  
XX PR 13-SEP-2002; 2002US-00323739.  
XX PA (HYSE-) HYSEQ INC.  
XX PI Tang Yt, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;  
PI Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang D;  
PI Haley-Vicente D;  
XX WPI; 2003-354603/33.  
XX N-PSDB; ADI21334.  
PT New polynucleotides and secreted proteins, useful for treating myeloid or  
PT lymphoid cell disorders, in bone cartilage, tendon, ligament and nerve  
PT tissue growth or regeneration, in wound healing, and in tissue repair and  
PT replacement.  
XX Example 3; SEQ ID NO 805; 156pp; English.

XX The invention relates to an isolated polynucleotide encoding a  
CC polypeptide with biological activity. The polynucleotides and  
CC polypeptides are useful in diagnostics, forensics, gene mapping,  
CC identification of mutations responsible for genetic disorders and other  
CC traits, to assess biodiversity, as nutritional sources or supplements.

CC The polynucleotides may also be used as molecular weight markers,  
CC chromosome markers or map related gene positions, or as an antigen to  
CC raise anti-DNA antibodies or elicit immune response. The polypeptides are  
CC useful for raising antibodies, as markers for tissues in which the  
CC corresponding polypeptide is expressed, for re-engineering damaged or  
CC diseased tissues, for treating myeloid or lymphoid cell disorders, in  
CC bone cartilage, tendon, ligament and/or nerve tissue growth or  
CC regeneration, in wound healing, in tissue repair and replacement, in  
CC healing of burns, incisions and ulcers, and in treating cancer. The  
CC present sequence represents the amino acid sequence of a novel human  
CC polypeptide.  
XX SQ Sequence 527 AA;

Query Match 100.0%; Score 2218; DB 7; Length 527;  
Best Local Similarity 100.0%; Pred. No. 3e-211;  
Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ALSFPQAGHDEGPGSGWAAKGTVRGNRRRARESPGHVSEPDRTQLSQDLGGGTLAMDTL 60  
DB 45 ALSFPQAGHDEGPGSGWAAKGTVRGNRRRARESPGHVSEPDRTQLSQDLGGGTLAMDTL 104  
QY 61 PDNRTRVVDNHSYVSRLYGSPSEPHSRELVDAEANRSQVKIHTILSNTHROASRVVL 120  
DB 105 PDNRTRVVDNHSYVSRLYGSPSEPHSRELVDAEANRSQVKIHTILSNTHROASRVVL 164  
QY 121 SFDPFFYGHPLRQITTIATGGFIHMDVTHRLMTATQYVAPLMAFNFGYSDNSTVYVFDN 180  
DB 165 SFDPFFYGHPLRQITTIATGGFIHMDVTHRLMTATQYVAPLMAFNFGYSDNSTVYVFDN 224  
QY 181 GTVFVQWDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHPVKTGLS 240  
DB 225 GTVFVQWDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHPVKTGLS 284  
QY 241 DAFMLNPSDPVPESRRRSIFEYHRIELDPKVTSMGSAVEFTPLPTCLOHRSCDACMSSD 300  
DB 285 DAFMLNPSDPVPESRRRSIFEYHRIELDPKVTSMGSAVEFTPLPTCLOHRSCDACMSSD 344  
QY 301 LTFNCSCWHLQRCSSGFDYRQEWMDYGCQAEGRMCEDFQDEHDSASPDTSFSPYD 360  
DB 345 LTFNCSCWHLQRCSSGFDYRQEWMDYGCQAEGRMCEDFQDEHDSASPDTSFSPYD 404  
QY 361 GDLTTSSSLFIDSLTTEDDTKLNPNYAGDGLQNNLSPKTKGTPVHLGTI 410  
DB 405 GDLTTSSSLFIDSLTTEDDTKLNPNYAGDGLQNNLSPKTKGTPVHLGTI 454

RESULT 6

ADI21553  
ID ADI21553 standard; protein; 527 AA.  
XX AC ADI21553;  
XX DT 15-APR-2004 (first entry)  
XX DE Novel human polypeptide #32.  
XX KW forensic; nutritional source; damaged tissue; diseased tissue;  
KW myeloid cell disorder; lymphoid cell disorder;  
KW bone cartilage tissue growth; tendon tissue growth;  
KW ligament tissue growth; nerve tissue growth; regeneration; wound healing;  
KW tissue repair; tissue replacement; burn; incision; ulcer; cancer; human.  
XX OS Homo sapiens.  
XX PN WO2003025148-A2.  
XX PD 27-MAR-2003.  
XX PF 19-SEP-2002; 2002WO-US029964.  
XX PR 19-SEP-2001; 2001US-0323739P.  
XX PR 13-SEP-2002; 2002US-00323739.



XX (HYSE-) HYSEQ INC.  
PA Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;  
PI Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang D;  
PI Haley-Vicente D;  
XX WPI; 2003-354603/33.  
DR N-PSDB; ADI21333.  
XX New polynucleotides and secreted proteins, useful for treating myeloid or  
PT lymphoid cell disorders, in bone cartilage, tendon, ligament and nerve  
PT tissue growth or regeneration, in wound healing, and in tissue repair and  
PT replacement.  
XX  
PS Example 3; SEQ ID NO 804; 156pp; English.  
XX  
CC The invention relates to an isolated polynucleotide encoding a  
CC polypeptide with biological activity. The polynucleotides and  
CC polypeptides are useful in diagnostics, forensics, gene mapping,  
CC identification of mutations responsible for genetic disorders and other  
CC traits, to assess biodiversity, as nutritional sources or supplements.  
CC The polynucleotides may also be used as molecular weight markers,  
CC chromosome markers or map related gene positions, or as an antigen to  
CC raise anti-DNA antibodies or elicit immune response. The polypeptides are  
CC useful for raising antibodies, as markers for tissues in which the  
CC corresponding polypeptide is expressed, for re-engineering damaged or  
CC diseased tissues, for treating myeloid or lymphoid cell disorders, in  
CC bone cartilage, tendon, ligament and/or nerve tissue growth or  
CC regeneration, in wound healing, in tissue repair and replacement, in  
CC healing of burns, incisions and ulcers, and in treating cancer. The  
CC present sequence represents the amino acid sequence of a novel human  
CC polypeptide.  
XX  
SQ Sequence 527 AA;

Query Match 100.0%; Score 2218; DB 7; Length 527;  
Best Local Similarity 100.0%; Pred. No. 3e-211;  
Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ALSPPQAGHDEGPGSGWAAKGTVRGNRRARESPGHVSEPDRTQLSQDLGGGTAMDTL 60  
Db 45 ALSPPQAGHDEGPGSGWAAKGTVRGNRRARESPGHVSEPDRTQLSQDLGGGTAMDTL 104  
Qy 61 PDNTRVVEDNHSYVSRLYGSPSPHRELVDAEANRSQVKIHTILSNTHROASRVVL 120  
Db 105 PDNTRVVEDNHSYVSRLYGSPSPHRELVDAEANRSQVKIHTILSNTHROASRVVL 164  
Qy 121 SFDPFPYGHPLRQITTIATGGIFMGDVIHRMLTATQYVAPLMAFNPGYSNNTVVYFDN 180  
Db 165 SFDPFPYGHPLRQITTIATGGIFMGDVIHRMLTATQYVAPLMAFNPGYSNNTVVYFDN 224  
Qy 181 GTVFVQWQDHVYVLCQWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSSQHPVKTLGSL 240  
Db 225 GTVFVQWQDHVYVLCQWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSSQHPVKTLGSL 284  
Qy 241 DAFMILNPSDPVPSRRRSIFEYHRIELDPKSVTMSAVEFTPTCLQHRSCDACMSSD 300  
Db 285 DAFMILNPSDPVPSRRRSIFEYHRIELDPKSVTMSAVEFTPTCLQHRSCDACMSSD 344  
Qy 301 LTFNCSWCHVLQRCSSGDFRVRQEMWYGCQAEGRCMCEQFQEDHDSAPDTSFSPYD 360  
Db 345 LTFNCSWCHVLQRCSSGDFRVRQEMWYGCQAEGRCMCEQFQEDHDSAPDTSFSPYD 404  
Qy 361 GDLTTTSSLSFLDLSLTDEDDTKLNPYAGDGLQNNLSPKTKGTPVHLGTI 410  
Db 405 GDLTTTSSLSFLDLSLTDEDDTKLNPYAGDGLQNNLSPKTKGTPVHLGTI 454

RESULT 7  
ABB90723  
ID ABB90723 standard; protein; 1002 AA.  
XX

AC ABB90723;  
XX  
XX 30-MAY-2002 (first entry)  
XX  
XX Human Tumour Endothelial Marker polypeptide SEQ ID NO 179.  
DE  
XX Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic;  
KW normal endothelial marker; pan-endothelial marker; immunostimulant;  
KW antiangiogenic; tumour; neoangiogenesis; vascularised tumour;  
KW polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;  
XX psoriasis.  
XX Homo sapiens.  
OS  
XX WO200210217-A2.  
FN  
XX 07-FEB-2002.  
PD  
XX 01-AUG-2001; 2001WO-US024031.  
PF  
XX 02-AUG-2000; 2000US-0222599P.  
PR  
XX 11-AUG-2000; 2000US-0224360P.  
PR  
XX 11-APR-2001; 2001US-0282850P.  
XX (UYJO ) UNIV JOHNS HOPKINS.  
PA  
XX St Croix B, Kinzler KW, Vogelstein B;  
PI  
XX WPI; 2002-291856/33.  
DR  
XX An isolated molecule comprising an antibody variable region which  
PT specifically binds to an extracellular domain of a tumor endothelial  
PT marker (TEM) protein, useful for inhibiting tumor growth.  
XX  
XX Disclosure; Page 125-128; 331pp; English.  
XX  
CC The invention relates to an isolated molecule comprising an antibody  
CC variable region which specifically binds to an extracellular domain of a  
CC tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740,  
CC ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM  
CC proteins have cytostatic, immunostimulant and antiangiogenic activity.  
CC They are useful for inhibiting tumour growth, neoangiogenesis in subjects  
CC bearing a vascularised tumour, polycystic kidney disease, diabetic  
CC retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM  
CC genes and the encoded proteins (ABL92075-ABL92141 and ABB90721-ABB90789)  
CC are disclosed, as are marker oligonucleotide sequences: tumour  
CC endothelial markers (TEM) ABL91936-ABL92041 and ABL92143-ABL92191; normal  
CC endothelial markers (NEM) ABL92042-ABL92074; and pan-endothelial markers  
CC (PEM) ABL91903-ABL91995  
XX  
SQ Sequence 1002 AA;

Query Match 100.0%; Score 2218; DB 5; Length 1002;  
Best Local Similarity 100.0%; Pred. No. 8e-211;  
Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ALSPPQAGHDEGPGSGWAAKGTVRGNRRARESPGHVSEPDRTQLSQDLGGGTAMDTL 60  
Db 520 ALSPPQAGHDEGPGSGWAAKGTVRGNRRARESPGHVSEPDRTQLSQDLGGGTAMDTL 579  
Qy 61 PDNTRVVEDNHSYVSRLYGSPSPHRELVDAEANRSQVKIHTILSNTHROASRVVL 120  
Db 580 PDNTRVVEDNHSYVSRLYGSPSPHRELVDAEANRSQVKIHTILSNTHROASRVVL 639  
Qy 121 SFDPFPYGHPLRQITTIATGGIFMGDVIHRMLTATQYVAPLMAFNPGYSNNTVVYFDN 180  
Db 640 SFDPFPYGHPLRQITTIATGGIFMGDVIHRMLTATQYVAPLMAFNPGYSNNTVVYFDN 699  
Qy 181 GTVFVQWQDHVYVLCQWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSSQHPVKTLGSL 240  
Db 700 GTVFVQWQDHVYVLCQWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSSQHPVKTLGSL 759  
Qy 241 DAFMILNPSDPVPSRRRSIFEYHRIELDPKSVTMSAVEFTPTCLQHRSCDACMSSD 300

Db 760 DAFMLNPSDPVPSRRRSIFEYHRIELDPKVTSMASVEFTPLPTCLQHRSCDACWSSD 819  
Qy 301 LTFNCSWCHVLQRCSSGFDRIYQWMDYGCQAQAEGRMCEDFQDEHDSASPDTSFSPYD 360  
Db 820 LTFNCSWCHVLQRCSSGFDRIYQWMDYGCQAQAEGRMCEDFQDEHDSASPDTSFSPYD 879  
Qy 361 GDLTTSSSLFIDSLTTEDDTKLNPAAGDGLQNNLSPKTKGTPVHLGTI 410  
Db 880 GDLTTSSSLFIDSLTTEDDTKLNPAAGDGLQNNLSPKTKGTPVHLGTI 929

RESULT 8  
ABU54430  
ID ABU54430 standard; protein; 1002 AA.  
XX AC ABU54430;  
XX DT 12-MAR-2003 (first entry)  
XX DE Human tumour endothelial marker TEM 8.  
XX KW Human; endothelial cell; EC; tumour endothelial cell; TEM; NEM;  
KW Tumour endothelial marker; normal endothelial marker; PEM;  
KW Pan-endothelial marker; polycystic kidney disease; psoriasis;  
KW diabetic retinopathy; rheumatoid arthritis; tumour angiogenesis;  
KW neoangiogenesis; immune response; cytostatic; antidiabetic;  
KW ophthalmological; antirheumatic; antiarthritic; antipeoriatic.  
XX OS Homo sapiens.  
XX PN WO200283874-A2.  
XX PD 24-OCT-2002.  
XX PF 10-APR-2002; 2002WO-US008253.  
XX PR 11-APR-2001; 2001US-0282850P.  
XX PR 06-FEB-2002; 2002US-0354262P.  
XX PA (UYJO ) UNIV JOHNS HOPKINS.  
XX PI Carson-Walter E, St Croix B, Kinzler KW, Vogelstein B;  
XX DR WPI; 2003-093016/08.  
XX DR N-FSDB; ABX72003.  
XX PT New purified human transmembrane protein, designated as tumor endothelial  
PT marker (TEM) 3, useful for detecting, diagnosing or treating tumors,  
PT polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis or  
PT psoriasis.  
XX PS Disclosure; Page 122-124; 374pp; English.  
XX CC The present invention relates to a novel method for the isolation of  
CC endothelial cells (ECs), and the identification of genes expressed in  
CC normal and tumour ECs. Tumour endothelial marker (TEM), normal  
CC endothelial marker (NEM), and pan-endothelial marker (PEM) genes are  
CC identified in human ECs. The human EC marker proteins and the  
CC polynucleotide sequences encoding them are useful for detecting,  
CC diagnosing or treating tumours as well as polycystic kidney disease,  
CC diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are also  
CC useful for inhibiting neoangiogenesis or tumour angiogenesis, for  
CC inducing an immune response to tumour endothelial cells in a patient, or  
CC for identifying candidate drugs for treating tumours. The present  
CC sequence represents a human TEM or NEM protein of the invention  
XX SQ Sequence 1002 AA;  
Query Match 100.0%; Score 2218; DB 6; Length 1002;  
Best Local Similarity 100.0%; Pred. No. 8e-211;  
Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALSPQPCAGHDEGPGGAAKGTVRGNRRRARESPGHVSEPDRTQLSQDLGGGTLAMDTL 60  
Db 520 ALSPQPCAGHDEGPGGAAKGTVRGNRRRARESPGHVSEPDRTQLSQDLGGGTLAMDTL 579  
Qy 61 PDNRTRVVDNHSYYSRLYGPSPHSRELWVDVAEANRSQVKIHTILSNTHROASRVVL 120  
Db 580 PDNRTRVVDNHSYYSRLYGPSPHSRELWVDVAEANRSQVKIHTILSNTHROASRVVL 639  
Qy 121 SFDPFPYGHPLROITITATGGFIWGDVTHRMLTATQYVAPLMANFNPGYSDNSTVYFDN 180  
Db 640 SFDPFPYGHPLROITITATGGFIWGDVTHRMLTATQYVAPLMANFNPGYSDNSTVYFDN 699  
Qy 181 GTVFVQWDHVLQGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPRISSQHSPVKTGLS 240  
Db 700 GTVFVQWDHVLQGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPRISSQHSPVKTGLS 759  
Qy 241 DAFMLNPSDPVPSRRRSIFEYHRIELDPKVTSMASVEFTPLPTCLQHRSCDACWSSD 300  
Db 760 DAFMLNPSDPVPSRRRSIFEYHRIELDPKVTSMASVEFTPLPTCLQHRSCDACWSSD 819  
Qy 301 LTFNCSWCHVLQRCSSGFDRIYQWMDYGCQAQAEGRMCEDFQDEHDSASPDTSFSPYD 360  
Db 820 LTFNCSWCHVLQRCSSGFDRIYQWMDYGCQAQAEGRMCEDFQDEHDSASPDTSFSPYD 879  
Qy 361 GDLTTSSSLFIDSLTTEDDTKLNPAAGDGLQNNLSPKTKGTPVHLGTI 410  
Db 880 GDLTTSSSLFIDSLTTEDDTKLNPAAGDGLQNNLSPKTKGTPVHLGTI 929

RESULT 9  
ADI21064  
ID ADI21064 standard; protein; 488 AA.  
XX AC ADI21064;  
XX DT 15-APR-2004 (first entry)  
XX DE Novel human protein #39.  
XX KW forensic; nutritional source; damaged tissue; diseased tissue;  
KW myeloid cell disorder; lymphoid cell disorder;  
KW bone cartilage tissue growth; tendon tissue growth;  
KW ligament tissue growth; nerve tissue growth; regeneration; wound healing;  
KW tissue repair; tissue replacement; burn; incision; ulcer; cancer; human.  
XX OS Homo sapiens.  
XX PN WO2003025148-A2.  
XX PD 27-MAR-2003.  
XX PF 19-SEP-2002; 2002WO-US029964.  
XX PR 19-SEP-2001; 2001US-0323739P.  
XX PR 13-SEP-2002; 2002US-00323739.  
XX PA (HYSE-) HYSEQ INC.  
XX PI Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QH, Wang J;  
PI Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang D;  
PI Haley-Vicente D;  
XX DR WPI; 2003-354603/33.  
XX DR N-FSDB; ADI21780.  
XX PT New polynucleotides and secreted proteins, useful for treating myeloid or  
PT lymphoid cell disorders, in bone cartilage, tendon, ligament and nerve  
PT tissue growth or regeneration, in wound healing, and in tissue repair and  
PT replacement.  
XX PS Claim 20; SEQ ID NO 315; 156pp; English.  
XX CC The invention relates to an isolated polynucleotide encoding a

CC polypeptide with biological activity. The polynucleotides and  
CC polypeptides are useful in diagnostics, forensics, gene mapping,  
CC identification of mutations responsible for genetic disorders and other  
CC traits, to assess biodiversity, as nutritional sources or supplements.  
CC The polynucleotides may also be used as molecular weight markers,  
CC chromosome markers or map related gene positions, or as an antigen to  
CC raise anti-DNA antibodies or elicit immune response. The polypeptides are  
CC useful for raising antibodies, as markers for tissues in which the  
CC corresponding polypeptide is expressed, for re-engineering damaged or  
CC diseased tissues, for treating myeloid or lymphoid cell disorders, in  
CC bone cartilage, tendon, ligament and/or nerve tissue growth or  
CC regeneration, in wound healing, in tissue repair and replacement, in  
CC healing of burns, incisions and ulcers, and in treating cancer. The  
CC present sequence represents the amino acid sequence of a novel human  
CC protein.  
XX  
XX  
SQ Sequence 488 AA;

Query Match 96.2%; Score 2134; DB 7; Length 488;  
Best Local Similarity 97.1%; Pred. NO. 6e-203;  
Matches 398; Conservative 0; Mismatches 0; Indels 12; Gaps 1;  
QY 1 ALSPPGAGHDEGPGSGAAAGTGVGNRRARSPGHVSEPDRTQLSODLGGGTAMDTL 60  
DB 18 ALSPPGAGHDEGPGSGAAAGTGVGNRRARSPGHVSEPDRTQLSODLGGGTAMDTL 77  
QY 61 PDNTRVVEDNHSYVSRLYGSPSPHRSRELWVDAEANRSQVKIHTILSNTHRQASRVVL 120  
DB 78 PDNTRVVEDNHSYVSRLYGSPSPHRSRELWVDAEANRSQVKIHTILSNTHRQASRVVL 137  
QY 121 SFDPFFYGHPLRQITATGGIFMGDVIRHMLTATQYVAPLMAFNPGYSNSTVVYFDN 180  
DB 138 SFDPFFYGHPLRQITATGGIFMGDVIRHMLTATQYVAPLMAFNPGYSNSTVVYFDN 197  
QY 181 GTVFVQWDHYVLOGWEDKGSFTFOALHHDGRIVFAYPEIAPMSVPEISSQHPVKTGLS 240  
DB 198 GTVFVQWDHYVLOGWEDKGSFTFOALHHDGRIVFAYPEIAPMSVPEISSQHPVKTGLS 257  
QY 241 DAFMLNPSDPVPESRRSIFFEYHRIELDPKVTSMASVETPTLCLQHRSCDACMSSD 300  
DB 258 DAFMLNPSDPVPESRRSIFFEYHRIELDPKVTSMASVETPTLCLQHRSCDACMSSD 317  
QY 301 LTFNCSWCHVLQRCSSGPDYRQEMWYGCQAEGRCMCEFDQEDHDSASPDTSFSPYD 360  
DB 318 LTFNCSWCHVLQRCSSGPDYRQEMWYGCQAEGRCMCEFDQEDHDSASPDTSFSPYD 377  
QY 361 GDLTFTSSSLFDSLTFTEDDTKLNFPYAGDGLQNNLSPKTKGTPVHLGTI 410  
DB 378 GDLTFTSSSLFDSLTFTEDDTKLNFPYAGDGLQNNLSPKTKGTPVHLGTI 415

RESULT 10  
AAB43131  
ID AAB43131 standard; protein; 400 AA.  
AC AAB43131;  
XX  
XX 08-FEB-2001 (first entry)  
XX Human ORFX ORF2895 polypeptide sequence SEQ ID NO:5790.  
DE  
DE Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;  
KW vulnery; antipariatic; antiparkinsonian; nortropic; neuroprotective;  
KW anticonvulsant; osteopathic; antilathritic; immunosuppressant; cardiant;  
KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;  
KW hypotensive; dermatological; immunosuppressive; antiinflammatory;  
KW antiviral; antibacterial; antifungal; antineumatic; antithyroid;  
KW antianaemic; gene therapy; cancer; proliferative disorder; hypertension;  
KW neurodegenerative disorder; osteoarthritis; graft vs host disease;  
KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;  
KW cholesterol ester storage; systemic lupus erythematosus; infection;  
KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;  
KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;

KW bone damage; cartilage damage; antiinflammatory disease; coagulation;  
KW thrombosis; contraceptive.  
XX Homo sapiens.  
XX WO2000058473-A2.  
XX 05-OCT-2000.  
XX 31-MAR-2000; 2000WO-US008621.  
XX 31-MAR-1999; 99US-0127607P.  
XX 02-APR-1999; 99US-0127636P.  
XX 05-APR-1999; 99US-0127728P.  
XX 30-MAR-2000; 2000US-00540763.  
XX (CURA-) CURAGEN CORP.  
XX Shimkets RA, Leach M;  
XX WPI; 2000-602362/57.  
XX N-PSDB; AAC77340.  
XX Novel nucleic acids and peptides derived from open reading frame X,  
XX useful for treating e.g. cancers, proliferative disorders,  
XX neurodegenerative disorders and cardiovascular disease.  
XX Claim 11; Page 4955; 5507pp; English.  
XX AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,  
XX which represent the human ORFX open reading frames 1 to 3161. The ORFX  
XX sequences have activities such as: cytostatic; hepatotropic; vulnery;  
XX antipariatic; antiparkinsonian; nortropic; neuroprotective; osteopathic;  
XX anticonvulsant; antilathritic; immunosuppressant; immunostimulant;  
XX cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive;  
XX dermatological; immunosuppressive; antiinflammatory; antibacterial;  
XX antiviral; antifungal; antineumatic; antithyroid; and antianaemic. The  
XX sequences can be used for determining the presence of or predisposition  
XX to, or preventing or treating pathological conditions associated with an  
XX ORFX-associated disorder. The nucleic acids can be used to express ORFX  
XX proteins in gene therapy vectors. The proteins and nucleic acids may be  
XX used to treat cancers, proliferative disorders, neurodegenerative  
XX disorders, osteoarthritis, graft vs host disease, cardiovascular disease,  
XX diabetes mellitus, hypertension, hypothyroidism, cholesterol ester  
XX storage, systemic lupus erythematosus, severe combined immunodeficiency  
XX (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune  
XX disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and  
XX cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to  
XX enhance coagulation; to inhibit thrombosis; and as a contraceptive  
XX  
SQ Sequence 400 AA;

Query Match 86.7%; Score 1924; DB 3; Length 400;  
Best Local Similarity 100.0%; Pred. NO. 3.6e-182;  
Matches 354; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ALSPPGAGHDEGPGSGAAAGTGVGNRRARSPGHVSEPDRTQLSODLGGGTAMDTL 60  
DB 46 ALSPPGAGHDEGPGSGAAAGTGVGNRRARSPGHVSEPDRTQLSODLGGGTAMDTL 105  
QY 61 PDNTRVVEDNHSYVSRLYGSPSPHRSRELWVDAEANRSQVKIHTILSNTHRQASRVVL 120  
DB 106 PDNTRVVEDNHSYVSRLYGSPSPHRSRELWVDAEANRSQVKIHTILSNTHRQASRVVL 165  
QY 121 SFDPFFYGHPLRQITATGGIFMGDVIRHMLTATQYVAPLMAFNPGYSNSTVVYFDN 180  
DB 166 SFDPFFYGHPLRQITATGGIFMGDVIRHMLTATQYVAPLMAFNPGYSNSTVVYFDN 225  
QY 181 GTVFVQWDHYVLOGWEDKGSFTFOALHHDGRIVFAYPEIAPMSVPEISSQHPVKTGLS 240  
DB 226 GTVFVQWDHYVLOGWEDKGSFTFOALHHDGRIVFAYPEIAPMSVPEISSQHPVKTGLS 285  
QY 241 DAFMLNPSDPVPESRRSIFFEYHRIELDPKVTSMASVETPTLCLQHRSCDACMSSD 300

Db 286 DAFMLNPSDPVPSRRSIFEHRIELDPKVTSMASVEFTPLTCLQHRSCDACMSSD 345  
 Qy 301 LTFNCSCWCHVLQRCSSGFDYRQEMWMDYGCAQEAEGRMCEDFQDEHDSASPD 354  
 Db 346 LTFNCSCWCHVLQRCSSGFDYRQEMWMDYGCAQEAEGRMCEDFQDEHDSASPD 399

## RESULT 11

ABB90783  
 ID ABB90783 standard; protein; 500 AA.  
 AC ABB90783;  
 XX  
 XX 30-MAY-2002 (first entry)  
 DT Mouse Tumour Endothelial Marker polypeptide SEQ ID NO 297.  
 DE Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic;  
 KW normal endothelial marker; pan-endothelial marker; immunostimulant;  
 KW antiangiogenic; tumour; neoangiogenesis; vascularised tumour;  
 KW polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;  
 KW psoriasis.  
 XX  
 XX Mus musculus.  
 OS  
 XX WO200210217-A2.  
 FN  
 XX 07-FEB-2002.  
 PD  
 XX 01-AUG-2001; 2001WO-US024031.  
 PP  
 XX 02-AUG-2000; 2000US-0222599P.  
 PR 11-AUG-2000; 2000US-0224360P.  
 PR 11-APR-2001; 2001US-022850P.  
 XX  
 XX (UWJO ) UNIV JOHNS HOPKINS.  
 PA  
 XX St Croix B, Kinzler KW, Vogelstein B;  
 PI WPI; 2002-291856/33.  
 DR N-PSDB; ABL92136.  
 DR  
 XX An isolated molecule comprising an antibody variable region which  
 PT specifically binds to an extracellular domain of a tumor endothelial  
 PT marker (TEM) protein, useful for inhibiting tumor growth.  
 XX  
 XX Disclosure; Page 301-302; 331pp; English.  
 PS  
 XX The invention relates to an isolated molecule comprising an antibody  
 CC variable region which specifically binds to an extracellular domain of a  
 CC tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740,  
 CC ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM  
 CC proteins have cytostatic, immunostimulant and antiangiogenic activity.  
 CC They are useful for inhibiting tumour growth, neoangiogenesis in subjects  
 CC bearing a vascularised tumour, polycystic kidney disease, diabetic  
 CC retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM  
 CC genes and the encoded proteins (ABL92073-ABL92141 and ABB90721-ABB90789)  
 CC are disclosed, as are marker oligonucleotide sequences: tumour  
 CC endothelial markers (TEM) ABL91996-ABL92041 and ABL92143-ABL92191; normal  
 CC endothelial markers (NEM) ABL92042-ABL92074; and pan-endothelial markers  
 CC (PEM) ABL91903-ABL91995  
 XX  
 XX Sequence 500 AA;

Query Match 81.1%; Score 1799.5; DB 5; Length 500;  
 Best Local Similarity 80.7%; Pred. No. 1.2e-169;  
 Matches 331; Conservative 39; Mismatches 39; Indels 1; Gaps 1;  
 Qy 1 ALSPOGAGHDEGPGSGWAAGTGVGNRRRARESPGHVSEPDRTQLSODLGGGTLAMD 60  
 Db 19 ALSPATPAGHNEGQDSAWTAKRTROGWRRRPRESPAQLKPGKTLQSLDGLGSLAIDL 78

Qy 61 PDNRTRVEDNHSYVSRSLYGPSEPHSRELWVDVAEANRSQVKIHTILSNTHQASRVVL 120  
 Db 79 PDNRTRVEDNHNHYVSRVYGPGEKQSDLWVDLAVANRSHVKIHRILSSSHRQASRVVL 138  
 Qy 121 SFDPFFYGHPLRQITTIATGGFIEMGDVIRHMLTATQYVAPLMAFNPNFGYSDNSTVYFDN 180  
 Db 139 SFDPFFYGHPLRQITTIATGGFIEMGDMLHRLMTATQYVAPLMAFNPNFGYSDNSTVYFDN 198  
 Qy 181 GTVPVQWHDHYVLOGWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHHPVKTGLS 240  
 Db 199 GTVPVQWHDHYVLOGWEDKGSFTFOAALHHDGRIVFAYKEIPMAVLDISSAQHPVKAGLS 258  
 Qy 241 DAFMLNPSDPVPSRRSIFEHRIELDPKVTSMASVEFTPLTCLQHRSCDACMSSD 300  
 Db 259 DAFMLNPSFEVPESQRRTIFEYHRVELDSKITTTSAVEFTPLTCLQHQSCDTCVSSN 318  
 Qy 301 LTFNCSCWCHVLQRCSSGFDYRQEMWMDYGCAQEAEGRMCEDFQDEHDSASPDTSFSPYD 360  
 Db 319 LTFNCSCWCHVLQRCSSGFDYRQEWLTYGCAQEAEGKTCEDFQDDSHYSASPDSSFSFPFN 378  
 Qy 361 GDLTTSSTSLFIDSLTTEDDTKLNPYAGDGLQNNLSPKTKGTPVHLGTI 410  
 Db 379 GD-STTSSSLFIDSLATTEDDTKLNPYAEGDGLPDHSPKSKGPPVHLGTI 427

## RESULT 12

ABB90729  
 ID ABB90729 standard; protein; 500 AA.  
 AC ABB90729;  
 XX  
 XX 30-MAY-2002 (first entry)  
 DT Mouse Tumour Endothelial Marker polypeptide SEQ ID NO 192.  
 DE Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic;  
 KW normal endothelial marker; pan-endothelial marker; immunostimulant;  
 KW antiangiogenic; tumour; neoangiogenesis; vascularised tumour;  
 KW polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;  
 KW psoriasis.  
 XX  
 XX Mus musculus.  
 OS  
 XX WO200210217-A2.  
 FN  
 XX 07-FEB-2002.  
 PD  
 XX 01-AUG-2001; 2001WO-US024031.  
 PP  
 XX 02-AUG-2000; 2000US-0222599P.  
 PR 11-AUG-2000; 2000US-0224360P.  
 PR 11-APR-2001; 2001US-022850P.  
 XX  
 XX (UWJO ) UNIV JOHNS HOPKINS.  
 PA  
 XX St Croix B, Kinzler KW, Vogelstein B;  
 PI WPI; 2002-291856/33.  
 DR  
 XX An isolated molecule comprising an antibody variable region which  
 PT specifically binds to an extracellular domain of a tumor endothelial  
 PT marker (TEM) protein, useful for inhibiting tumor growth.  
 XX  
 XX Disclosure; Page 146-147; 331pp; English.  
 PS  
 XX The invention relates to an isolated molecule comprising an antibody  
 CC variable region which specifically binds to an extracellular domain of a  
 CC tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740,  
 CC ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM  
 CC proteins have cytostatic, immunostimulant and antiangiogenic activity.  
 CC They are useful for inhibiting tumour growth, neoangiogenesis in subjects  
 CC bearing a vascularised tumour, polycystic kidney disease, diabetic  
 CC retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM  
 CC genes and the encoded proteins (ABL92073-ABL92141 and ABB90721-ABB90789)  
 CC are disclosed, as are marker oligonucleotide sequences: tumour  
 CC endothelial markers (TEM) ABL91996-ABL92041 and ABL92143-ABL92191; normal  
 CC endothelial markers (NEM) ABL92042-ABL92074; and pan-endothelial markers  
 CC (PEM) ABL91903-ABL91995  
 XX  
 XX Sequence 500 AA;

CC genes and the encoded proteins (ABL92075-ABL92141 and ABB90721-ABB90789) are disclosed, as are marker oligonucleotide sequences: tumour  
CC endothelial markers (TEM) ABL91996-ABL92041 and ABL92143-ABL92191; normal  
CC endothelial markers (NEM) ABL92042-ABL92074; and pan-endothelial markers  
CC (PEM) ABL91903-ABL91995  
XX  
XX Sequence 500 AA;  
Query Match 81.1%; Score 1799.5; DB 5; Length 500;  
Best Local Similarity 80.7%; Pred. No. 1.2e-169;  
Matches 331; Conservative 39; Mismatches 39; Indels 1; Gaps 1;  
QY 1 ALSPOGAGHDEGPGSGWAAGTGVGNRRRARESPGHVSEPDRTQLSQDLGGGTAMDTL 60  
Db 19 ALSPATPAGHNEGQDSAWTAKTRQGWRRPRESPAQVLKPKGTQLSQDLGGGSLAIDTL 78  
QY 61 PDNTRRVVEDNHSYVSRLYGSPHRELWVDVAENRSQVKIHTILSNTHRQASRVVL 120  
Db 79 PDNTRRVVEDNHSYVSRVYGGEGKQSDLDVAVNRSHVKIHLSSHRQASRVVL 138  
QY 121 SFDPFFYGHPLRQITATGGFIFMGDVHRMLTATQYVAPLMANFNPGYSDNSTVYVFDN 180  
Db 139 SFDPFFYGHPLRQITATGGFIFMGDLHRLMTATQYVAPLMANFNPGYSDNSTVYVFDN 198  
QY 181 GTVFVQWDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHPVKTGLS 240  
Db 199 GTVFVQWDHVLQDREDRGSFTFOAALHRDGRIVFGYKEIPMAVLDISSAQHPVKAGLS 258  
QY 241 DAFMLNPSDPVPSRRRSIPEYHRIELDPKSVTSMSAVEFTPLTCLQHSRCDACMSD 300  
Db 259 DAFMLNPSPEVPESQRTIPEYHVELDSSKITTTSAVEFTPLTCLQHSRCDTCVSN 318  
QY 301 LTFNCSWCHVLQRCSSGFDYRQEWMDYGCQAEGKTCEDFQDDSHYSASPDSSFSFPN 360  
Db 319 LTFNCSWCHVLQRCSSGFDYRQEWLTYGCAQAEAGKTCEDFQDDSHYSASPDSSFSFPN 378  
QY 361 GDLTTSSSLFIDSITTEDDTKLNYPAGDGLQNNLSPKTKGTPVHLGTI 410  
Db 379 GD-STTSSSLFIDSITTEDDTKLNYPAGDGLPDHSSPKSKGPPVHLGTI 427  
RESULT 13  
ABU54436  
ID ABU54436 standard; protein; 500 AA.  
XX  
XX AC ABU54436;  
XX  
XX DT 12-MAR-2003 (first entry)  
XX  
XX DE Mouse tumour endothelial marker TEM 7.  
XX  
XX KW Mouse; endothelial cell; EC; tumour endothelial cell; TEM; NEM;  
KW Tumour endothelial marker; normal endothelial marker; PEM;  
KW pan-endothelial marker; polycystic kidney disease; psoriasis;  
KW diabetic retinopathy; rheumatoid arthritis; tumour angiogenesis;  
KW neovascularization; immune response; cytostatic; antidiabetic;  
KW ophthalmological; antirheumatic; antiarthritic; antipsoriatic.  
XX  
XX OS Mus musculus.  
XX  
XX PN WO200283874-A2.  
XX  
XX PD 24-OCT-2002.  
XX  
XX PF 10-APR-2002; 2002WO-US008253.  
XX  
XX PR 11-APR-2001; 2001US-0282850P.  
XX  
XX PR 06-FEB-2002; 2002US-0354262P.  
XX  
XX PA (UWJO ) UNIV JOHNS HOPKINS.  
XX  
XX PI Carson-Walter E, St Croix B, Kinzler KW, Vogelstein B;  
XX

DR WPI; 2003-093016/08.  
DR N-PSDB; ABX72008.  
XX  
XX PT New purified human transmembrane protein, designated as tumor endothelial  
XX marker (TEM) 3, useful for detecting, diagnosing or treating tumors, or  
XX polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis or  
XX psoriasis.  
XX  
XX PS Disclosure; Page 147-148; 374pp; English.  
XX  
XX CC The present invention relates to a novel method for the isolation of  
XX endothelial cells (ECs), and the identification of genes expressed in  
XX normal and tumor ECs. Tumour endothelial marker (TEM), normal  
XX endothelial marker (NEM), and pan-endothelial marker (PEM) genes are  
XX identified in human ECs. The human EC marker proteins and the  
XX polynucleotide sequences encoding them are useful for detecting,  
XX diagnosing or treating tumors as well as polycystic kidney disease,  
XX diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are also  
XX useful for inhibiting neovascularization or tumour angiogenesis, for  
XX inducing an immune response to tumour endothelial cells in a patient, or  
XX for identifying candidate drugs for treating tumors. The present  
XX sequence represents a mouse TEM protein  
XX  
XX Sequence 500 AA;  
Query Match 81.1%; Score 1799.5; DB 6; Length 500;  
Best Local Similarity 80.7%; Pred. No. 1.2e-169;  
Matches 331; Conservative 39; Mismatches 39; Indels 1; Gaps 1;  
QY 1 ALSPOGAGHDEGPGSGWAAGTGVGNRRRARESPGHVSEPDRTQLSQDLGGGTAMDTL 60  
Db 19 ALSPATPAGHNEGQDSAWTAKTRQGWRRPRESPAQVLKPKGTQLSQDLGGGSLAIDTL 78  
QY 61 PDNTRRVVEDNHSYVSRLYGSPHRELWVDVAENRSQVKIHTILSNTHRQASRVVL 120  
Db 79 PDNTRRVVEDNHSYVSRVYGGEGKQSDLDVAVNRSHVKIHLSSHRQASRVVL 138  
QY 121 SFDPFFYGHPLRQITATGGFIFMGDVHRMLTATQYVAPLMANFNPGYSDNSTVYVFDN 180  
Db 139 SFDPFFYGHPLRQITATGGFIFMGDLHRLMTATQYVAPLMANFNPGYSDNSTVYVFDN 198  
QY 181 GTVFVQWDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHPVKTGLS 240  
Db 199 GTVFVQWDHVLQDREDRGSFTFOAALHRDGRIVFGYKEIPMAVLDISSAQHPVKAGLS 258  
QY 241 DAFMLNPSDPVPSRRRSIPEYHRIELDPKSVTSMSAVEFTPLTCLQHSRCDACMSD 300  
Db 259 DAFMLNPSPEVPESQRTIPEYHVELDSSKITTTSAVEFTPLTCLQHSRCDTCVSN 318  
QY 301 LTFNCSWCHVLQRCSSGFDYRQEWMDYGCQAEGKTCEDFQDDSHYSASPDSSFSFPN 360  
Db 319 LTFNCSWCHVLQRCSSGFDYRQEWLTYGCAQAEAGKTCEDFQDDSHYSASPDSSFSFPN 378  
QY 361 GDLTTSSSLFIDSITTEDDTKLNYPAGDGLQNNLSPKTKGTPVHLGTI 410  
Db 379 GD-STTSSSLFIDSITTEDDTKLNYPAGDGLPDHSSPKSKGPPVHLGTI 427  
RESULT 14  
ABU54490  
ID ABU54490 standard; protein; 500 AA.  
XX  
XX AC ABU54490;  
XX  
XX DT 12-MAR-2003 (first entry)  
XX  
XX DE Mouse tumour endothelial marker mTEM 9.  
XX  
XX KW Mouse; endothelial cell; EC; tumour endothelial cell; TEM; NEM;  
KW Tumour endothelial marker; normal endothelial marker; PEM;  
KW pan-endothelial marker; polycystic kidney disease; psoriasis;  
KW diabetic retinopathy; rheumatoid arthritis; tumour angiogenesis;  
KW neovascularization; immune response; cytostatic; antidiabetic;  
KW

KW ophthalmological; antirheumatic; antiarthritic; antipsoriatic.

XX Mus sp.

XX WO200283874-A2.

XX 24-OCT-2002.

XX 10-APR-2002; 2002WO-US008253.

XX 11-APR-2001; 2001US-0282850P.

XX 06-FEB-2002; 2002US-0354262P.

XX (UWJ) UNIV JOHNS HOPKINS.

XX Carson-Walter E, St Croix B, Kinzler KW, Vogelstein B;

XX WPI; 2003-093016/08.

XX N-PSDB; ABX72061.

XX New purified human transmembrane protein, designated as tumor endothelial marker (TEM) 3, useful for detecting, diagnosing or treating tumors, polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis or psoriasis.

XX Disclosure; Page 339-340; 374pp; English.

XX The present invention relates to a novel method for the isolation of endothelial cells (ECs), and the identification of genes expressed in normal and tumor ECs. Tumor endothelial marker (TEM), normal endothelial marker (NEM), and pan-endothelial marker (PEM) genes are identified in human ECs. The human EC marker proteins and the polynucleotide sequences encoding them are useful for detecting, diagnosing or treating tumors as well as polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are also useful for inhibiting neoangiogenesis or tumor angiogenesis, for inducing an immune response to tumor endothelial cells in a patient, or for identifying candidate drugs for treating tumors. The present sequence represents a mouse TEM protein

XX Sequence 500 AA;

Query Match 81.1%; Score 1799.5; DB 6; Length 500;  
Best Local Similarity 80.7%; Pred. No. 1.2e-169;  
Matches 331; Conservative 39; Mismatches 33; Indels 1; Gaps 1;

QY 1 ALSPOGAGHDEGPGSGWAAKTGVGNRRARESPGHVSEPDRTQLSDLGGLAMDTL 60

DB 19 ALSPATPAGHNEGQDSAWTAKTRQCGWRRRPRESPAQLKPKTKQLSDLGGSIAIDTL 78

QY 61 PDNRTRVVDNHSYVSLYGPSEPHSRELWVDVAENRSOVKIHITLSNTHRSRVVL 120

DB 79 PDNRTRVVDNHSYVSLYGPSEPHSRELWVDVAENRSOVKIHITLSNTHRSRVVL 138

QY 121 SFDPFFYGHPLRQITATGGTIFMGDVIHRLMTATQYVAPLMANFNPQYSDNSTVYFDN 180

DB 139 SFDPFFYGHPLRQITATGGTIFMGDVIHRLMTATQYVAPLMANFNPQYSDNSTVYFDN 198

QY 181 GTVFVQWDHYVQWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHPVKTLGS 240

DB 199 GTVFVQWDHYVQWEDKGSFTFOAALHHDGRIVFAYKEIPMAVLDISSAQHPVKAGLS 258

QY 241 DAFMLTNSPDVPESSRSIPEYHRIELDPKVTSMASAVEFTPLTCLOHRSQCDACWSSD 300

DB 259 DAFMLTNSPEVPESSQRTIPEYHRIELDPKVTSMASAVEFTPLTCLOHRSQCDVSSN 318

QY 301 LTFNCSWCHVLQRCSSGDRVQWMDYGCQAEGRCMEDFQDBDHDSDASPDTSFSPYD 360

DB 319 LTFNCSWCHVLQRCSSGDRVQWMDYGCQAEGRKCEDFQDDSHYSASPDSSFPFN 378

QY 361 GDLTTSSSLFIDSITLTTDDTKLNPYAGDGLQNNLSPKTKGTPVHLGTI 410

DB 379 GD-STTSSSLFIDSITLTTDDTKLNPYAGDGLPDHSSPKSKGPPVHLGTI 427

RESULT 15

AAB85400

ID AAB85400 standard; protein; 431 AA.

XX AAB85400;

XX 17-SEP-2001 (first entry)

XX Tumour endothelial marker 7 precursor protein.

XX Stem cell growth factor-like polypeptide; leukemia; hemophilia; human; degenerative disease; Alzheimer's disease; nutritional supplement; cytosolic; neuroprotective; hemostatic; antisense-therapy; gene-therapy; tumour endothelial marker 7 precursor protein.

XX Homo sapiens.

XX WO200153500-A1.

XX 26-JUL-2001.

XX 23-DEC-2000; 2000WO-US035260.

XX 23-DEC-1999; 99US-00471275.

XX 21-JAN-2000; 2000US-00488725.

XX 07-APR-2000; 2000US-00545714.

XX 11-APR-2000; 2000US-00547358.

XX (HYSE-) HYSEQ INC.

XX Labat J, Tang YT, Drmanac RT, Liu C, Lee J, Mize NK, Childs J;

XX Chao C;

XX WPI; 2001-451909/48.

XX Isolated polypeptide with stem cell growth factor-like activity for treatment of leukemia, hemophilia, and degenerative diseases like Alzheimer's disease and to generate new tissues and organs.

XX Example 4; Page 149-150; 154pp; English.

XX The invention provides novel human stem cell growth factor-like polypeptides and polynucleotides encoding them. The polypeptides having stem cell growth factor-like activity, can be expressed by standard recombinant methodology. The polynucleotides and polypeptides can be used to induce differentiation of embryonic and adult stem cells to give rise to different cell types. They may also be used in the treatment of leukemia, hemophilia, and degenerative diseases like Alzheimer's disease. They may also be utilized to generate new tissues and organs that may aid patients in need of transplants. They can also be used as nutritional supplements. The present sequence represents a tumour endothelial marker 7 precursor protein, homologous to a stem cell growth factor-like polypeptide

XX Sequence 431 AA;

Query Match 80.9%; Score 1795; DB 4; Length 431;

Best Local Similarity 94.2%; Pred. No. 2.8e-169;

Matches 343; Conservative 0; Mismatches 7; Indels 14; Gaps 3;

QY 55 LAMDTLPDNRTRVVDNHSYVSLYGPSEPHSRELWVDVAENRSOVKIHITLSNTHRQ 114

DB 1 LAMDTLPDNRTRVVDNHSYVSLYGPSEPHSRELWVDVAENRSOVKIHITLSNTHRQ 60

QY 115 ASRVVLSFDPFFYGHPLRQITATGGTIFMGDVIHRLMTATQYVAPLMANFNPQYSDNST 174

DB 61 ASRVVLSFDPFFYGHPLRQITATGGTIFMGDVIHRLMTATQYVAPLMANFNPQYSDNST 120

QY 175 VVYFDNGTIVFVQWHDHYVQWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHP 234

DB 121 VVYFDNGTIVFVQWHDHYVQWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHP 180

QY 235 VKTGLSDAFMILNPSDPVPESSRRRSIFEYHRIELDPKVTSMASAVEFTPLPTCLOHRSCD 294  
Db |||||  
181 VKTGLSDAFMILNPSDPVPESSRRRSIFEYHRIELDPKVTSMASAVEFTPLPTCLOHRSCD 240  
QY 295 ACMSSDLTFNCSCWCHVLCRCSSGFDYRQEW-MDYGCAQAEGRMCEDFOD-----ED 346  
Db |||||  
241 ACMSSDLTFNCSCWCHVLCRCSSGFDYRQEWDTGTWGCQAEAG-----QDVRGLPGNRT 294  
QY 347 HDSASPDTSFSPYDGLTTTSSSLFIDSLLTTEDDTKLNPNYAGDGLQNNLSPKTKGTVPVH 406  
Db |||||  
295 TTASASPDTSFSPYDGLTTTSSSLFIDSLLTTEDDTKLNPNYAGDGLQNNLSPKTKGTVPVH 354  
QY 407 LGTI 410  
Db ||||  
355 LGTI 358

Search completed: January 28, 2005, 22:05:04  
Job time : 132.231 secs



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Db 78 PDRNRVVEDNHSYVSLYGPSPHRELVDAEANRSQVKIHTILSNTHRQASRVVL 137  
Qy 121 SFDPFFYGHPLRQITATGGFIFMGDVIRHMLTATQYVAPLMAFNPGYSNNTVYFDN 180  
Db 138 SFDPFFYGHPLRQITATGGFIFMGDVIRHMLTATQYVAPLMAFNPGYSNNTVYFDN 197  
Qy 181 GTVFVQWQDHVYVQWEDKGSFTFOAALHHDGRIVFAVKEIPMSVPEISSQHPVKTGLS 240  
Db 198 GTVFVQWQDHVYVQWEDKGSFTFOAALHHDGRIVFAVKEIPMSVPEISSQHPVKTGLS 257  
Qy 241 DAFMILNPSDPVPSRRRSIFEYHRIELDPKVTSMASAVEFTPLTCLQHRSCDACMSD 300  
Db 258 DAFMILNPSDPVPSRRRSIFEYHRIELDPKVTSMASAVEFTPLTCLQHRSCDACMSD 317  
Qy 301 LTFNCNCHVLRQCSGFDYRQEWMDYGCQAEGRMCEDFQDEHDSASPDTSFSPYD 360  
Db 318 LTFNCNCHVLRQCSGFDYRQEWMDYGCQAEGRMCEDFQDEHDSASPDTSFSPYD 377  
Qy 361 GDLTTSSSLFIDSLTTEDDTKLNPAAGDGLQNNLSPKTKGTPVHLGTI 410  
Db 378 GDLTTSSSLFIDSLTTEDDTKLNPAAGDGLQNNLSPKTKGTPVHLGTI 427

## RESULT 2

US-10-435-696-79  
; Sequence 79, Application US/10435696  
; Publication No. US20040018525A1  
; GENERAL INFORMATION:  
; APPLICANT: Wittz, Ralph  
; APPLICANT: Munnes, Marc  
; APPLICANT: Kallabis, Harald  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE PREDICTION, DIAGNOSIS, PROGNOSIS  
; TITLE OF INVENTION: PREVENTION AND TREATMENT OF MALIGNANT NEOPLASIA  
; FILE REFERENCE: Lea 36 108  
; CURRENT APPLICATION NUMBER: US/10/435,696  
; CURRENT FILING DATE: 2003-05-09  
; PRIOR APPLICATION NUMBER: EP03003112.4  
; PRIOR FILING DATE: 2003-02-13  
; PRIOR APPLICATION NUMBER: EP02010291.9  
; PRIOR FILING DATE: 2002-05-21  
; NUMBER OF SEQ ID NOS: 314  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 79  
; LENGTH: 500  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-435-696-79

Query Match 100.0%; Score 2218; DB 15; Length 500;  
Best Local Similarity 100.0%; Pred. No. 1.5e-203;  
Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ALSPOGAGHDEGPGSGWAAKGTVRGNRRARESPGHVSEPDRTQLSQDLGGGTLMADTL 60  
Db 18 ALSPOGAGHDEGPGSGWAAKGTVRGNRRARESPGHVSEPDRTQLSQDLGGGTLMADTL 77  
Qy 61 PDRNRVVEDNHSYVSLYGPSPHRELVDAEANRSQVKIHTILSNTHRQASRVVL 120  
Db 78 PDRNRVVEDNHSYVSLYGPSPHRELVDAEANRSQVKIHTILSNTHRQASRVVL 137  
Qy 121 SFDPFFYGHPLRQITATGGFIFMGDVIRHMLTATQYVAPLMAFNPGYSNNTVYFDN 180  
Db 138 SFDPFFYGHPLRQITATGGFIFMGDVIRHMLTATQYVAPLMAFNPGYSNNTVYFDN 197  
Qy 181 GTVFVQWQDHVYVQWEDKGSFTFOAALHHDGRIVFAVKEIPMSVPEISSQHPVKTGLS 240  
Db 198 GTVFVQWQDHVYVQWEDKGSFTFOAALHHDGRIVFAVKEIPMSVPEISSQHPVKTGLS 257  
Qy 241 DAFMILNPSDPVPSRRRSIFEYHRIELDPKVTSMASAVEFTPLTCLQHRSCDACMSD 300  
Db 258 DAFMILNPSDPVPSRRRSIFEYHRIELDPKVTSMASAVEFTPLTCLQHRSCDACMSD 317  
Qy 301 LTFNCNCHVLRQCSGFDYRQEWMDYGCQAEGRMCEDFQDEHDSASPDTSFSPYD 360

Db 318 LTFNCNCHVLRQCSGFDYRQEWMDYGCQAEGRMCEDFQDEHDSASPDTSFSPYD 377  
Qy 361 GDLTTSSSLFIDSLTTEDDTKLNPAAGDGLQNNLSPKTKGTPVHLGTI 410  
Db 378 GDLTTSSSLFIDSLTTEDDTKLNPAAGDGLQNNLSPKTKGTPVHLGTI 427  
RESULT 3  
US-10-474-794-230  
; Sequence 230, Application US/10474794  
; Publication No. US20040213793A1  
; GENERAL INFORMATION:  
; APPLICANT: Carson-Walter, Eleanor  
; APPLICANT: St. Croix, Brad  
; APPLICANT: Vogelstein, Bert  
; APPLICANT: Kinzler, Kenneth  
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS  
; FILE REFERENCE: 1107.00179  
; CURRENT APPLICATION NUMBER: US/10/474,794  
; CURRENT FILING DATE: 2003-10-14  
; PRIOR FILING DATE: 2001-04-11  
; PRIOR APPLICATION NUMBER: 60/282,850  
; PRIOR FILING DATE: 2001-08-01  
; PRIOR APPLICATION NUMBER: 60/308,829  
; NUMBER OF SEQ ID NOS: 359  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 230  
; LENGTH: 500  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-474-794-230

Query Match 100.0%; Score 2218; DB 17; Length 500;  
Best Local Similarity 100.0%; Pred. No. 1.5e-203;  
Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ALSPOGAGHDEGPGSGWAAKGTVRGNRRARESPGHVSEPDRTQLSQDLGGGTLMADTL 60  
Db 18 ALSPOGAGHDEGPGSGWAAKGTVRGNRRARESPGHVSEPDRTQLSQDLGGGTLMADTL 77  
Qy 61 PDRNRVVEDNHSYVSLYGPSPHRELVDAEANRSQVKIHTILSNTHRQASRVVL 120  
Db 78 PDRNRVVEDNHSYVSLYGPSPHRELVDAEANRSQVKIHTILSNTHRQASRVVL 137  
Qy 121 SFDPFFYGHPLRQITATGGFIFMGDVIRHMLTATQYVAPLMAFNPGYSNNTVYFDN 180  
Db 138 SFDPFFYGHPLRQITATGGFIFMGDVIRHMLTATQYVAPLMAFNPGYSNNTVYFDN 197  
Qy 181 GTVFVQWQDHVYVQWEDKGSFTFOAALHHDGRIVFAVKEIPMSVPEISSQHPVKTGLS 240  
Db 198 GTVFVQWQDHVYVQWEDKGSFTFOAALHHDGRIVFAVKEIPMSVPEISSQHPVKTGLS 257  
Qy 241 DAFMILNPSDPVPSRRRSIFEYHRIELDPKVTSMASAVEFTPLTCLQHRSCDACMSD 300  
Db 258 DAFMILNPSDPVPSRRRSIFEYHRIELDPKVTSMASAVEFTPLTCLQHRSCDACMSD 317  
Qy 301 LTFNCNCHVLRQCSGFDYRQEWMDYGCQAEGRMCEDFQDEHDSASPDTSFSPYD 360  
Db 318 LTFNCNCHVLRQCSGFDYRQEWMDYGCQAEGRMCEDFQDEHDSASPDTSFSPYD 377  
Qy 361 GDLTTSSSLFIDSLTTEDDTKLNPAAGDGLQNNLSPKTKGTPVHLGTI 410  
Db 378 GDLTTSSSLFIDSLTTEDDTKLNPAAGDGLQNNLSPKTKGTPVHLGTI 427

## RESULT 4

US-10-357-819-2  
; Sequence 2, Application US/10357819  
; Publication No. US20040259774A1  
; GENERAL INFORMATION:  
; APPLICANT: Alvarez, Enrique  
; APPLICANT: Edinger, Shlomit R.

APPLICANT: Gangolli, Esha A.  
APPLICANT: Gerlach, Valerie L.  
APPLICANT: Gorman, Linda  
APPLICANT: Guo, Xiaojia  
APPLICANT: Ji, Weizhen  
APPLICANT: Kekuda, Ramesh  
APPLICANT: Li, Li  
APPLICANT: Miller, Charles E.  
APPLICANT: Patturajan, Meera  
APPLICANT: Rastelli, Luca  
APPLICANT: Rieger, Daniel K.  
APPLICANT: Shenoy, Suresh G.  
APPLICANT: Shinkets, Richard A.  
APPLICANT: Spytek, Kimberly A.  
APPLICANT: Zhong, Mei  
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD  
FILE REFERENCE: 21402-538A  
CURRENT APPLICATION NUMBER: US/10/357,819  
CURRENT FILING DATE: 2003-02-03  
PRIOR FILING DATE: 09/520,781  
PRIOR FILING DATE: 2000-03-08  
PRIOR APPLICATION NUMBER: 09/584,411  
PRIOR FILING DATE: 2000-05-31  
PRIOR APPLICATION NUMBER: 09/783,436  
PRIOR FILING DATE: 2001-02-14  
PRIOR APPLICATION NUMBER: 10/085,198  
PRIOR FILING DATE: 2002-02-25  
PRIOR APPLICATION NUMBER: 60/353,301  
PRIOR FILING DATE: 2002-02-01  
PRIOR APPLICATION NUMBER: 60/355,099  
PRIOR FILING DATE: 2002-02-08  
PRIOR APPLICATION NUMBER: 60/356,424  
PRIOR FILING DATE: 2002-02-12  
PRIOR APPLICATION NUMBER: 60/358,239  
PRIOR FILING DATE: 2002-02-20  
PRIOR APPLICATION NUMBER: 60/358,608  
PRIOR FILING DATE: 2002-02-21  
PRIOR APPLICATION NUMBER: 60/359,367  
PRIOR FILING DATE: 2002-02-25  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 142  
SOFTWARE: CuraseqList version 0.1  
SEQ ID NO 2  
LENGTH: 500  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-357-819-2

Query Match 100.0%; Score 2218; DB 17; Length 500;  
Best Local Similarity 100.0%; Pred. No. 1.5e-203;  
Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALSPOGAGHDEGPGSGWAAKGTVRGWNRRARESPGHVSEPDRTQLSODLGGGTLMMDTL 60  
Db 18 ALSPOGAGHDEGPGSGWAAKGTVRGWNRRARESPGHVSEPDRTQLSODLGGGTLMMDTL 77  
Qy 61 PDRTRVVDNHSYVVSRLYGPSPHSELVWDAEANRSQVKIHTILSNTHROASRVVL 120  
Db 78 PDRTRVVDNHSYVVSRLYGPSPHSELVWDAEANRSQVKIHTILSNTHROASRVVL 137  
Qy 121 SPDFPFYGHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMAFNPCYSDNSTVYVFDN 180  
Db 138 SPDFPFYGHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMAFNPCYSDNSTVYVFDN 197  
Qy 181 GTVFVQWDHVLQWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHPVKTGLS 240  
Db 198 GTVFVQWDHVLQWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHPVKTGLS 257  
Qy 241 DAFMLNPSDPVPSRRRSIFEYHRIELDPKVTSMASAVEFTPLTCLQHRSCDACMSDD 300  
Db 258 DAFMLNPSDPVPSRRRSIFEYHRIELDPKVTSMASAVEFTPLTCLQHRSCDACMSDD 317

Qy 301 LTFNCSCWHLQRCSSGFDYRQWMDYGCQAQEAEGRMCEDFQDEHDSASPDTSFSFYD 360  
Db 318 LTFNCSCWHLQRCSSGFDYRQWMDYGCQAQEAEGRMCEDFQDEHDSASPDTSFSFYD 377  
Qy 361 GDLTTTSSSLFIDSLLTTTDDTKLNPYAGGDLQNNLSFKTKGTPVHLGTI 410  
Db 378 GDLTTTSSSLFIDSLLTTTDDTKLNPYAGGDLQNNLSFKTKGTPVHLGTI 427

RESULT 5  
US-09-918-715-179  
; Sequence 179, Application US/09918715  
; Publication No. US20030017157A1  
; GENERAL INFORMATION:  
; APPLICANT: Brad St. Croix  
; APPLICANT: Kenneth Kinzler  
; APPLICANT: Bert Vogelstein  
; TITLE OF INVENTION: ENDOPHELIAL CELL EXPRESSION PATTERNS  
; FILE REFERENCE: 1107.00134  
; CURRENT APPLICATION NUMBER: US/09/918,715  
; CURRENT FILING DATE: 2001-08-01  
; PRIOR FILING DATE: 60/222,599  
; PRIOR FILING DATE: 2000-08-02  
; PRIOR APPLICATION NUMBER: 60/224,360  
; PRIOR FILING DATE: 2000-08-11  
; PRIOR APPLICATION NUMBER: 60/282,850  
; PRIOR FILING DATE: 2000-04-11  
; NUMBER OF SEQ ID NOS: 358  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 179  
; LENGTH: 1002  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-918-715-179

Query Match 100.0%; Score 2218; DB 10; Length 1002;  
Best Local Similarity 100.0%; Pred. No. 4.5e-203;  
Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALSPOGAGHDEGPGSGWAAKGTVRGWNRRARESPGHVSEPDRTQLSODLGGGTLMMDTL 60  
Db 520 ALSPOGAGHDEGPGSGWAAKGTVRGWNRRARESPGHVSEPDRTQLSODLGGGTLMMDTL 579  
Qy 61 PDRTRVVDNHSYVVSRLYGPSPHSELVWDAEANRSQVKIHTILSNTHROASRVVL 120  
Db 580 PDRTRVVDNHSYVVSRLYGPSPHSELVWDAEANRSQVKIHTILSNTHROASRVVL 639  
Qy 121 SPDFPFYGHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMAFNPCYSDNSTVYVFDN 180  
Db 640 SPDFPFYGHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMAFNPCYSDNSTVYVFDN 699  
Qy 181 GTVFVQWDHVLQWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHPVKTGLS 240  
Db 700 GTVFVQWDHVLQWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHPVKTGLS 759  
Qy 241 DAFMLNPSDPVPSRRRSIFEYHRIELDPKVTSMASAVEFTPLTCLQHRSCDACMSDD 300  
Db 760 DAFMLNPSDPVPSRRRSIFEYHRIELDPKVTSMASAVEFTPLTCLQHRSCDACMSDD 819  
Qy 301 LTFNCSCWHLQRCSSGFDYRQWMDYGCQAQEAEGRMCEDFQDEHDSASPDTSFSFYD 360  
Db 820 LTFNCSCWHLQRCSSGFDYRQWMDYGCQAQEAEGRMCEDFQDEHDSASPDTSFSFYD 879  
Qy 361 GDLTTTSSSLFIDSLLTTTDDTKLNPYAGGDLQNNLSFKTKGTPVHLGTI 410  
Db 880 GDLTTTSSSLFIDSLLTTTDDTKLNPYAGGDLQNNLSFKTKGTPVHLGTI 929

RESULT 6  
US-10-474-794-179  
; Sequence 179, Application US/10474794  
; Publication No. US20040213793A1  
; GENERAL INFORMATION:



```
; GENERAL INFORMATION:
; APPLICANT: Juan, Todd
; APPLICANT: Bass, Michael B.
; APPLICANT: Oliner, John
; TITLE OF INVENTION: Tumor Endothelial Marker 7a Molecules and Uses Thereof
; FILE REFERENCE: 01-072-A
; CURRENT APPLICATION NUMBER: US/10/156,487A
; CURRENT FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: 60/293,852
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-156-487A-5

Query Match      94.4%; Score 2093; DB 14; Length 502;
Best Local Similarity 95.0%; Pred. No. 1.5e-191;
Matches 397; Conservative 0; Mismatches 7; Indels 14; Gaps 3;

Qy 1 ALSPOGAGHDEGPGSGWAAKGTVRGNRRARESPGHVSEPDRTQLSQDLGGGTLMADTL 60
Db 18 ALSPOGAGHDEGPGSGWAAKGTVRGNRRARESPGHVSEPDRTQLSQDLGGGTLMADTL 77
Qy 61 PDNTRVVEDNHSYVSRLYGSPSEPHSRELWVDVAEANRSQVKIHTILSNTHRQASRVYL 120
Db 78 PDNTRVVEDNHSYVSRLYGSPSEPHSRELWVDVAEANRSQVKIHTILSNTHRQASRVYL 137
Qy 121 SFDPFPYGHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMAFNPGYSDNSTVYVFDN 180
Db 138 SFDPFPYGHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMAFNPGYSDNSTVYVFDN 197
Qy 181 GTVFVQWQDHYVQLQGWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHPVKTGLS 240
Db 198 GTVFVQWQDHYVQLQGWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHPVKTGLS 257
Qy 241 DAFMLNPSDPVPSRRRSIFEYHRIELDPKVTSMGSAVEFTPLTCLQHRSCDACMSSD 300
Db 258 DAFMLNPSDPVPSRRRSIFEYHRIELDPKVTSMGSAVEFTPLTCLQHRSCDACMSSD 317
Qy 301 LTFNCWCHVQLQRCSSGFDYRQEWMDYGCQAQEAEGMCEDFQD-----EHDGASP 352
Db 318 LTFNCWCHVQLQRCSSGFDYRQEWMDYGCQAQEAEGMCEDFQD-----QDVRGLPGMRTTTSASP 371
Qy 353 DTSPSPYDGLTTSSSLFIDSLLTTEDDTKLNYPAGDGLQNNLSPKTKGTPVHLGTI 410
Db 372 DTSPSPYDGLTTSSSLFIDSLLTTEDDTKLNYPAGDGLQNNLSPKTKGTPVHLGTI 429

RESULT 9
US-09-918-715-192
; Sequence 192, Application US/09918715
; Publication No. US20030017157A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/09/918,715
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 192
; LENGTH: 500
; TYPE: PRT
; ORGANISM: Mouse
US-09-918-715-297

Query Match      81.1%; Score 1799,5; DB 10; Length 500;
Best Local Similarity 80.7%; Pred. No. 2.2e-163;
Matches 331; Conservative 39; Mismatches 39; Indels 1; Gaps 1;

Qy 1 ALSPOGAGHDEGPGSGWAAKGTVRGNRRARESPGHVSEPDRTQLSQDLGGGTLMADTL 60
Db 19 ALSPATPAGHNEGQDSAWTAKRTQGWRRRPRESPAQVLKPGKTQLSQDLGGGSLAIDTL 78
Qy 61 PDNTRVVEDNHSYVSRLYGSPSEPHSRELWVDVAEANRSQVKIHTILSNTHRQASRVYL 120
Db 79 PDNTRVVEDNHSYVSRLYGSPSEPHSRELWVDVAEANRSQVKIHTILSNTHRQASRVYL 138
Qy 121 SFDPFPYGHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMAFNPGYSDNSTVYVFDN 180
Db 139 SFDPFPYGHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMAFNPGYSDNSTVYVFDN 198
Qy 181 GTVFVQWQDHYVQLQGWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHPVKTGLS 240
Db 199 GTVFVQWQDHYVQLQGWEDKGSFTFOAALHHDGRIVFAYKEIPMAVLDISSAQHPVKAGLS 258
Qy 241 DAFMLNPSDPVPSRRRSIFEYHRIELDPKVTSMGSAVEFTPLTCLQHRSCDACMSSD 300
Db 259 DAFMLNPSDPVPSRRRSIFEYHRIELDPKVTSMGSAVEFTPLTCLQHRSCDACMSSD 318
Qy 301 LTFNCWCHVQLQRCSSGFDYRQEWMDYGCQAQEAEGMCEDFQD-----EHDGASP 352
Db 319 LTFNCWCHVQLQRCSSGFDYRQEWMDYGCQAQEAEGMCEDFQD-----EHDGASP 378
Qy 361 GDLTSTSSSLFIDSLLTTEDDTKLNYPAGDGLQNNLSPKTKGTPVHLGTI 410
Db 379 GDLTSTSSSLFIDSLLTTEDDTKLNYPAGDGLQNNLSPKTKGTPVHLGTI 427

RESULT 10
US-09-918-715-297
; Sequence 297, Application US/09918715
; Publication No. US20030017157A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/09/918,715
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 297
; LENGTH: 500
; TYPE: PRT
; ORGANISM: Mouse
US-09-918-715-297

Query Match      81.1%; Score 1799,5; DB 10; Length 500;
Best Local Similarity 80.7%; Pred. No. 2.2e-163;
Matches 331; Conservative 39; Mismatches 39; Indels 1; Gaps 1;

Qy 1 ALSPOGAGHDEGPGSGWAAKGTVRGNRRARESPGHVSEPDRTQLSQDLGGGTLMADTL 60
Db 19 ALSPATPAGHNEGQDSAWTAKRTQGWRRRPRESPAQVLKPGKTQLSQDLGGGSLAIDTL 78
Qy 61 PDNTRVVEDNHSYVSRLYGSPSEPHSRELWVDVAEANRSQVKIHTILSNTHRQASRVYL 120
Db 79 PDNTRVVEDNHSYVSRLYGSPSEPHSRELWVDVAEANRSQVKIHTILSNTHRQASRVYL 138
Qy 121 SFDPFPYGHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMAFNPGYSDNSTVYVFDN 180
Db 139 SFDPFPYGHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMAFNPGYSDNSTVYVFDN 198
Qy 181 GTVFVQWQDHYVQLQGWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHPVKTGLS 240
Db 199 GTVFVQWQDHYVQLQGWEDKGSFTFOAALHHDGRIVFAYKEIPMAVLDISSAQHPVKAGLS 258
Qy 241 DAFMLNPSDPVPSRRRSIFEYHRIELDPKVTSMGSAVEFTPLTCLQHRSCDACMSSD 300
Db 259 DAFMLNPSDPVPSRRRSIFEYHRIELDPKVTSMGSAVEFTPLTCLQHRSCDACMSSD 318
Qy 301 LTFNCWCHVQLQRCSSGFDYRQEWMDYGCQAQEAEGMCEDFQD-----EHDGASP 352
Db 319 LTFNCWCHVQLQRCSSGFDYRQEWMDYGCQAQEAEGMCEDFQD-----EHDGASP 378
Qy 361 GDLTSTSSSLFIDSLLTTEDDTKLNYPAGDGLQNNLSPKTKGTPVHLGTI 410
Db 379 GDLTSTSSSLFIDSLLTTEDDTKLNYPAGDGLQNNLSPKTKGTPVHLGTI 427
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Db 79 PDNRTRVEDNHNYYVSRVYGEKQSDQLWDLAVANRSHVKIHRILSSSHRQASRVVL 138  
Qy 121 SFDPFFYGHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMAFNPGYSNDSTVVYFDN 180  
Db 139 SFDPFFYGHPLRQITATGGFIFMGDMLHRMLTATQYVAPLMAFNPGYSNDSTVAYFDN 198  
Qy 181 GTVFVQWHDVYVLOGWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHVPKVTGLS 240  
Db 199 GTVFVQWHDVYVLOGWEDKGSFTFOAALHHDGRIVFAYKEIPMAVLDISSAQHPVKAGLS 258  
Qy 241 DAFMILNPSDPVPESSRRRSIFEYHRIELDPKSVTMSAVETPLPTCLQHRSCDACMSSD 300  
Db 259 DAFMILNPSPEVPESSRRRSIFEYHRIELDPKSVTMSAVETPLPTCLQHRSCDTCVSSN 318  
Qy 301 LTFNCSWCHVLQRCSSGDRYRQEWMDYGCQAEGRCMCEDFQDDSHYSASPDSSFSFPFN 360  
Db 319 LTFNCSWCHVLQRCSSGDRYRQEWMDYGCQAEGRCMCEDFQDDSHYSASPDSSFSFPFN 378  
Qy 361 GDLTTSSSLFIDSLLTTEDDTKLNPAAGDGLQNNLSPKTKGTPVHLGTI 410  
Db 379 GD-STTSSSLFIDSLLTTEDDTKLNPAAGDGLPDHSSSPKSGPPVHLGTI 427

## RESULT 11

US-10-156-487A-6  
; Sequence 6, Application US/10156487A  
; Publication No. US2003092025A1  
; GENERAL INFORMATION:  
; APPLICANT: Juan, Todd  
; APPLICANT: Bass, Michael B.  
; APPLICANT: Olinier, John  
; TITLE OF INVENTION: Tumor Endothelial Marker 7a Molecules and Uses Thereof  
; FILE REFERENCE: 01-072-A  
; CURRENT APPLICATION NUMBER: US/10/156,487A  
; CURRENT FILING DATE: 2002-09-10  
; PRIOR APPLICATION NUMBER: 60/293,852  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 500  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-156-487A-6

Query Match 81.1%; Score 1799.5; DB 14; Length 500;  
Best Local Similarity 80.7%; Pred. No. 2.2e-163;  
Matches 331; Conservative 39; Mismatches 39; Indels 1; Gaps 1;  
Qy 1 ALSPOGAGHDGPGSGWAAKGTVRGWNRRARSPGHVSEBPDRTQLSQDLGGGTLMADTLL 60  
Db 19 ALSPATPAGHNEGQDSAWTAKTRQGNRRRPRESPAQVLKPGKTQLSQDLGGGSLAIDTL 78  
Qy 61 PDNRTRVEDNHNYYVSRVYGEKRSQDLWDLAVANRSHVKIHRILSSSHRQASRVVL 120  
Db 79 PDNRTRVEDNHNYYVSRVYGEKRSQDLWDLAVANRSHVKIHRILSSSHRQASRVVL 138  
Qy 121 SFDPFFYGHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMAFNPGYSNDSTVVYFDN 180  
Db 139 SFDPFFYGHPLRQITATGGFIFMGDMLHRMLTATQYVAPLMAFNPGYSNDSTVAYFDN 198  
Qy 181 GTVFVQWHDVYVLOGWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHVPKVTGLS 240  
Db 199 GTVFVQWHDVYVLOGWEDKGSFTFOAALHHDGRIVFAYKEIPMAVLDISSAQHPVKAGLS 258  
Qy 241 DAFMILNPSDPVPESSRRRSIFEYHRIELDPKSVTMSAVETPLPTCLQHRSCDACMSSD 300  
Db 259 DAFMILNPSPEVPESSRRRSIFEYHRIELDPKSVTMSAVETPLPTCLQHRSCDTCVSSN 318  
Qy 301 LTFNCSWCHVLQRCSSGDRYRQEWMDYGCQAEGRCMCEDFQDDSHYSASPDSSFSFPFN 360  
Db 319 LTFNCSWCHVLQRCSSGDRYRQEWMDYGCQAEGRCMCEDFQDDSHYSASPDSSFSFPFN 378

Qy 361 GDLTTSSSLFIDSLLTTEDDTKLNPAAGDGLQNNLSPKTKGTPVHLGTI 410  
Db 379 GD-STTSSSLFIDSLLTTEDDTKLNPAAGDGLPDHSSSPKSGPPVHLGTI 427  
RESULT 12  
US-10-474-794-192  
; Sequence 192, Application US/10474794  
; Publication No. US20040213793A1  
; GENERAL INFORMATION:  
; APPLICANT: Carson-Walter, Eleanor  
; APPLICANT: St. Croix, Brad  
; APPLICANT: Vogelstein, Bert  
; APPLICANT: Kinzler, Kenneth  
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS  
; FILE REFERENCE: 1107.00179  
; CURRENT APPLICATION NUMBER: US/10/474,794  
; CURRENT FILING DATE: 2003-10-14  
; PRIOR APPLICATION NUMBER: 60/282,850  
; PRIOR FILING DATE: 2001-04-11  
; PRIOR APPLICATION NUMBER: 60/308,829  
; PRIOR FILING DATE: 2001-08-01  
; NUMBER OF SEQ ID NOS: 359  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 192  
; LENGTH: 500  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-474-794-192

Query Match 81.1%; Score 1799.5; DB 17; Length 500;  
Best Local Similarity 80.7%; Pred. No. 2.2e-163;  
Matches 331; Conservative 39; Mismatches 39; Indels 1; Gaps 1;  
Qy 1 ALSPOGAGHDGPGSGWAAKGTVRGWNRRARSPGHVSEBPDRTQLSQDLGGGTLMADTLL 60  
Db 19 ALSPATPAGHNEGQDSAWTAKTRQGNRRRPRESPAQVLKPGKTQLSQDLGGGSLAIDTL 78  
Qy 61 PDNRTRVEDNHNYYVSRVYGEKRSQDLWDLAVANRSHVKIHRILSSSHRQASRVVL 120  
Db 79 PDNRTRVEDNHNYYVSRVYGEKRSQDLWDLAVANRSHVKIHRILSSSHRQASRVVL 138  
Qy 121 SFDPFFYGHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMAFNPGYSNDSTVVYFDN 180  
Db 139 SFDPFFYGHPLRQITATGGFIFMGDMLHRMLTATQYVAPLMAFNPGYSNDSTVAYFDN 198  
Qy 181 GTVFVQWHDVYVLOGWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHVPKVTGLS 240  
Db 199 GTVFVQWHDVYVLOGWEDKGSFTFOAALHHDGRIVFAYKEIPMAVLDISSAQHPVKAGLS 258  
Qy 241 DAFMILNPSDPVPESSRRRSIFEYHRIELDPKSVTMSAVETPLPTCLQHRSCDACMSSD 300  
Db 259 DAFMILNPSPEVPESSRRRSIFEYHRIELDPKSVTMSAVETPLPTCLQHRSCDTCVSSN 318  
Qy 301 LTFNCSWCHVLQRCSSGDRYRQEWMDYGCQAEGRCMCEDFQDDSHYSASPDSSFSFPFN 360  
Db 319 LTFNCSWCHVLQRCSSGDRYRQEWMDYGCQAEGRCMCEDFQDDSHYSASPDSSFSFPFN 378  
Qy 361 GDLTTSSSLFIDSLLTTEDDTKLNPAAGDGLQNNLSPKTKGTPVHLGTI 410  
Db 379 GD-STTSSSLFIDSLLTTEDDTKLNPAAGDGLPDHSSSPKSGPPVHLGTI 427

## RESULT 13

US-10-474-794-297  
; Sequence 297, Application US/10474794  
; Publication No. US20040213793A1  
; GENERAL INFORMATION:  
; APPLICANT: Carson-Walter, Eleanor  
; APPLICANT: St. Croix, Brad  
; APPLICANT: Vogelstein, Bert  
; APPLICANT: Kinzler, Kenneth  
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS





Db 181 VKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKVTSMASAVEFTPLPTCLQHRSCD 240  
QY 295 ACMSSDLTFNCSWCHVLCRCSSGFDYRQEW-MDYGCAQEAEGRMCEDFQD-----ED 346  
Db 241 ACMSSDLTFNCSWCHVLCRCSSGFDYRQEW-MDYGCAQEAEGRMCEDFQD-----ED 346  
QY 347 HDSASPDTSFSPYDGLTTTSSSLFIDSLLTTEDDTKLNPNYAGDGLQNNLSPKTKGTPVH 406  
Db 295 TTSASPDTSFSPYDGLTTTSSSLFIDSLLTTEDDTKLNPNYAGDGLQNNLSPKTKGTPVH 354  
QY 407 LGTI 410  
Db 355 LGTI 358

Search completed: January 28, 2005, 22:19:20  
Job time : 113.059 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 28, 2005, 21:55:58 ; Search time 7.47922 Seconds  
(without alignments)  
1389.370 Million cell updates/sec

Title: US-09-918-715-230\_COPY\_137\_244  
Perfect score: 588  
Sequence: 1 LSFDFPYGHPRLQITATG.....LHHDGRIVFAYKEIPMSVPE 108

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_79.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	317.5	54.0	476	2 T19786	hypothetical prote
2	123	20.9	1161	1 S31213	nitrogen precursor
3	84	14.3	2120	2 T30243	alpha tectorin - c
4	83.5	14.2	1321	2 A60165	sodium channel pro
5	79	13.4	310	2 JC7853	L-fucose-specific
6	78	13.3	2155	2 T30197	alpha tectorin - m
7	73	12.4	1879	2 S74915	extracellular nucl
8	73	12.4	4436	2 E71086	hypothetical prote
9	68	11.6	324	2 A97918	3-oxoacyl-[acyl-ca
10	68	11.6	324	2 C95048	3-oxoacyl-[acyl-ca
11	68	11.6	337	2 S77723	vitamin B12 recept
12	67.5	11.5	356	2 JH0289	class I histocompa
13	67.5	11.5	535	2 S18606	phosphoenolpyruvat
14	67	11.4	392	2 JC4553	heme d1 synthesis
15	67	11.4	462	2 B82510	transporter, NacC
16	67	11.4	543	2 B84232	transport system p
17	67	11.4	614	1 QRECBT	vitamin B12 recept
18	67	11.4	614	2 A98241	hypothetical prote
19	67	11.4	614	2 P86088	hypothetical prote
20	66	11.2	330	2 H71981	hypothetical prote
21	66	11.2	365	2 T08679	procollagen-lysine
22	66	11.2	614	2 A80935	vitamin B12 recept
23	66	11.2	728	2 S59964	procollagen-lysine
24	65.5	11.1	2214	2 T16305	hypothetical prote
25	65	11.1	362	2 JH0288	class I histocompa
26	64	10.9	280	1 VPXRWN	outer capsid prote
27	64	10.9	280	1 VPXR16	outer capsid prote
28	64	10.9	401	2 A85758	probable oxidoredu
29	64	10.9	401	2 B64877	probable membrane

30	64	10.9	401	2 D90861	probable oxidoredu
31	64	10.9	424	2 B36109	pregnancy-specific
32	64	10.9	424	2 A34595	pregnancy-specific
33	64	10.9	609	2 A48290	reaction center co
34	64	10.9	609	2 T31454	reaction center co
35	64	10.9	776	1 VPXRW9	outer layer protei
36	64	10.9	1407	2 T28702	probable polyketid
37	63.5	10.8	337	2 G97742	cytochrome c oxida
38	63.5	10.8	390	2 G89877	conserved hypot het
39	63.5	10.8	506	2 A86899	lysine specific pe
40	63.5	10.8	606	2 B72412	glutamine-fructose
41	63	10.7	189	2 D71073	hypothetical prote
42	63	10.7	243	2 A95064	conserved hypot het
43	63	10.7	264	2 C97931	conserved hypot het
44	63	10.7	375	2 D90134	60S ribosomal prot
45	63	10.7	435	2 D33258	pregnancy-specific

ALIGNMENTS

RESULT 1

T19786  
hypothetical protein C36E8.3 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T19786  
R:Wilkinson, J.; Barlow, K.  
submitted to the EMBL Data Library, August 1994  
A:Reference number: Z19177  
A:Accession: T19786  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: DNA  
A:Residues: 1-476 <WIL>  
A:Cross-references: UNIPROT:Q18500; EMBL:Z35597; PIDN:CAA84646.1; GSPDB:GN00021; CESP:CC3  
C:Genetics:  
A:Experimental source: clone C36E8  
A:Map position: 3  
A:Gene: CESP:C36E8.3  
A:Introns: 23/1; 101/3; 152/3; 206/3; 235/1; 255/3; 320/1; 445/2  
C:Superfamily: Caenorhabditis elegans hypothetical protein C36E8.3

Query Match	54.0%	Score	317.5	DB 2	Length	476
Best Local Similarity	55.7%	Pred. No.	4.5e-26			
Matches	59	Conservative	19	Mismatches	27	Indels 1; Gaps 1;
Oy	1	LSDFPFGHPRLQITATG	GFIEMGVHRLMTATQVAPL	MANENPGYSDNSTVVYFD	60	
Db	156	LQFPPFYGHKMSNLTIATG	FIYIGDHSNWLAAQTIA	PLMANFHT-YLNSNIVYAD	214	
Oy	61	NGTVFVQWDRVYLQGWEDK	GSFTFQAALHHDGRIVFAY	KEIPMSV	106	
Db	215	DGELFVVEWRNVQLKEDK	DEHSFTFQILHKGNDIVFI	YKDVPI	260	

RESULT 2

S31213  
nitrogen precursor - sea squirt (Halocynthia roretzi)  
N:Alternate names: entactin  
C:Species: Halocynthia roretzi  
C>Date: 30-Sep-1993 #sequence\_revision 27-Feb-1997 #text\_change 09-Jul-2004  
C:Accession: S31213  
R:Nakae, H.; Sugano, M.; Ishimori, Y.; Endo, T.; Obinata, T.  
Eur. J. Biochem. 213, 11-19, 1993  
A:Title: Ascidian entactin/nitrogen. Implication of evolution by shuffling two kinds of  
A:Reference number: S31213; MUID:93238676; PMID:8477687  
A:Accession: S31213  
A:Molecule type: mRNA  
A:Residues: 1-1161 <NAK>  
A:Cross-references: UNIPROT:Q04901; EMBL:D14038; NID:G217363; PIDN:BAAO3127.1; PID:G2173  
C:Superfamily: Ascidian nitogen; EGF homology; LDL receptor YWTD-containing repeat homol  
C:Keywords: basement membrane; collagen binding; disulfide bond; duplication; extracellu  
F;1-20/Domain: signal sequence #status predicted <SIG>

F:21-1161/Product: nidogen #status predicted <MAT>  
F:274-306/Domain: EGF homology <EG1>  
F:560-574/Region: 3-residue repeats (R-P-V)  
F:603-673/Domain: thyroglobulin type I repeat homology <THY1>  
F:686-748/Domain: thyroglobulin type I repeat homology <THY2>  
F:752-819/Domain: thyroglobulin type I repeat homology <THY3>  
F:900-943/Domain: LDL receptor WYTD-containing repeat homology <YW1>  
F:944-986/Domain: LDL receptor WYTD-containing repeat homology <YW2>  
F:987-1031/Domain: LDL receptor WYTD-containing repeat homology <YW3>  
F:1032-1075/Domain: LDL receptor WYTD-containing repeat homology <YW4>  
F:1076-1114/Domain: LDL receptor WYTD-containing repeat homology <YW4>  
F:1129-1158/Domain: EGF homology <EG2>  
F:107,334,360,484/Binding site: carbohydrate (Asn) #status predicted

Query Match 20.9%; Score 123; DB 1; Length 1161;  
Best Local Similarity 28.0%; Pred. No. 7.7e-05;  
Matches 40; Conservative 18; Mismatches 41; Indels 44; Gaps 5;

Qy 1 LSPDFPPFYGHPLRQITTIATGGFIFM-----GDVIHRLTATQYVAPLMAN----- 45  
Db 47 LSMPIVFVDQKYDSVTVHTDGFITLNVGADTDGEVL-----LAPFMSDLDTLSG 97

Qy 46 --FNPGYSDNSTVYV-----FDNGTFVFWQDHVYLOGWEDKGSFTFQAA 88  
Db 98 DIFFREHKDNATIRANTDVREAFIETAGDFNAGSVFVVTWVKVQSASREDGVTFTQCI 157

Qy 89 LHHDGRIVFA---YKEIPMSVPE 108  
Db 158 VATDGAATFAIFLPQDGLAVGE 180

RESULT 3  
T30243  
alpha tectorin - chicken  
C:Species: Gallus gallus (chicken)  
C>Date: 02-Sep-2000 #sequence\_revision 02-Sep-2000 #text\_change 09-Jul-2004  
C:Accession: T30243  
R:Coutinho, P.; Goodyear, R.G.; Legan, P.K.; Richardson, G.P.  
Hear. Res. 130, 62-74, 1999

A:Title: Chick alpha tectorin : molecular cloning and expression during embryogenesis.  
A:Reference number: 220783; MUID:99251817; PMID:10320099  
A:Accession: T30243  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-2120 <COU>  
A:Cross-references: UNIPROT:Q9YH85; EMBL:AJ012287; NID:e1361091; PID:e1361092; PIDN:CAAO  
A:Note: non-collagenous protein only expressed in the inner ear

Query Match 14.3%; Score 84; DB 2; Length 2120;  
Best Local Similarity 27.1%; Pred. No. 2.3;  
Matches 38; Conservative 14; Mismatches 46; Indels 42; Gaps 8;

Qy 1 LSPDFPPFYGHPLRQITTIATGGFIFMGDVHRL-----MLTATQYVAPL-----MAN----- 45  
Db 51 LSVPFIFRSPYRTVYVNNNGVIGFNSLSVQFTPEAPPLADGRAFPVAPFCGDVANGIRGE 110

Qy 46 -----FNP---GYSDNSTVYFDN-----GTFVFWQDHVYLOGWEDKGSF-----TF 85  
Db 111 IYRESTNPPELLGSSKDIRKYFKDMASFSASWPIVTWESEVQPYG-----GSSSTPVPNTF 166

Qy 86 QAALHHDG---RIVFAYKEI 102  
Db 167 QAVLITDGVSSFAIFNYQEI 186

RESULT 4  
A60165  
sodium channel protein - fruit fly (Drosophila melanogaster) (fragments)  
C:Species: Drosophila melanogaster  
C>Date: 22-Jan-1993 #sequence\_revision 22-Jan-1993 #text\_change 09-Jul-2004  
C:Accession: S04029; A60165  
R:Salkoff, L.; Butler, A.; Scavarda, N.; Wei, A.  
Nucleic Acids Res. 15, 8569-8572, 1987

A:Title: Nucleotide sequence of the putative sodium channel gene from Drosophila: the fo  
A:Reference number: S04029; MUID:88040482; PMID:2444928  
A:Accession: S04029  
A:Molecule type: DNA  
A:Residues: 1-362;363-626;627-1321 <SAL>  
A:Cross-references: UNIPROT:Q27930; EMBL:X14394  
R:Salkoff, L.; Butler, A.; Wei, A.; Scavarda, N.; Giffen, K.; Ifune, C.; Goodman, R.; Ma:  
Science 237, 744-749, 1987  
A:Title: Genomic organization and deduced amino acid sequence of a putative sodium chann  
A:Reference number: A60165; MUID:87292090; PMID:2441469  
A:Accession: A60165  
A>Status: nucleic acid sequence not shown  
A:Molecule type: DNA  
A:Residues: 40-355;363-560,'P',562-626;632-1263 <SA2>  
A:Cross-references: EMBL:X14394  
A:Note: part of this sequence was confirmed by mRNA sequencing  
A:Note: the authors' translation is shown at position 561  
C:Genetics:  
A:Gene: FlyBase:NaCP60E  
A:Cross-references: FlyBase:FBgn0002920  
A:Introns: 237/2; 310/3; 362/3; 414/3; 471/3; 531/3; 581/1; 626/3; 751/2; 801/1; 908/1;  
Query Match 14.2%; Score 83.5; DB 2; Length 1321;  
Best Local Similarity 31.1%; Pred. No. 1.5;  
Matches 19; Conservative 12; Mismatches 25; Indels 5; Gaps 2;

Qy 9 GHPLRQITTIATGGFIFMGDVHRLTATQYVAPLMANFNPGYSDNSTVYFDNGTFVFWQ 68  
Db 1171 GHPLLAITYFT-SFI-----IISYMINVINMYITAILENFNOAHQEEIGIVEDDLEMPYIR 1235

Qy 69 W 69  
Db 1226 W 1226

RESULT 5  
JC7853  
L-fucose-specific lectin - Aspergillus oryzae  
C:Species: Aspergillus oryzae  
C>Date: 18-Nov-2002 #sequence\_revision 18-Nov-2002 #text\_change 09-Jul-2004  
C:Accession: JC7853; PC7191  
R:Ishida, H.; Moritani, T.; Hata, Y.; Kawato, A.; Suginami, K.; Abe, Y.; Imayasu, S.  
Biosci. Biotechnol. Biochem. 66, 1002-1008, 2002

A:Title: Molecular cloning and overexpression of fLeA gene encoding a fucose-specific le  
A:Reference number: JC7853; MUID:22087106; PMID:12092808  
A:Accession: JC7853  
A:Molecule type: DNA  
A:Residues: 1-310 <ISH>  
A:Cross-references: UNIPROT:Q8TGE0; DDBJ:AB072379  
A:Experimental source: strain OSI1018  
A:Accession: PC7191  
A:Molecule type: protein  
A:Residues: 132-147;148-177 <IS2>  
C:Comment: This protein, with ferrichrysin-affinity, has hemagglutination activity again  
C:Genetics:  
A:Gene: fLeA  
A:Introns: 12/1; 71/3; 143/1; 177/2

Query Match 13.4%; Score 79; DB 2; Length 310;  
Best Local Similarity 45.2%; Pred. No. 0.78;  
Matches 19; Conservative 5; Mismatches 14; Indels 4; Gaps 2;

Qy 45 NFNPGYSDNSTVYFDN--GTFVFWQDHVYLOGWEDKGSFT 84  
Db 219 NFNP GKSSIYMRIFYVNSDNTIWQVCWDHG--QG YHDKRTIT 258

RESULT 6  
T30197  
alpha tectorin - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T30197

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Qy      97 PAYKEIEMSVPE 108
      ||| ::| :
Db      220 FAIRDVAKSIQ 231

RESULT 10
C95048

```

3-oxoacyl-[acyl-carrier-protein] synthase III [imported] - Streptococcus pneumoniae (str  
C;Species: Streptococcus pneumoniae  
C;Date: 03-Aug-2001 #sequence\_revision 03-Aug-2001 #text\_change 09-Jul-2004  
C;Accession: C95048  
R;Tetelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid  
on, J.D.; Unayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfel,  
neon, T.; Hickey, E.K.; Holt, I.E.  
Science 293, 498-506, 2001  
A;Authors: Lofthus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,  
A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.  
A;Reference number: A95000; MUID:21357209; PMID:11463916  
A;Accession: C95048  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-324 <KUR>  
A;Cross-references: UNIPROT:Q9ANAL; GB:AE005672; PIDN:AAK74580.1; PID:g14971886; GSPDB:C  
A;Experimental source: strain TIGR4  
C;Genetics:  
A;Gene: SP0417  
C;Superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase III

Query Match 11.6%; Score 68; DB 2; Length 324;  
Best Local Similarity 23.5%; Pred. No. 12;  
Matches 31; Conservative 19; Mismatches 36; Indels 46; Gaps 7;

Qy 15 ITIATGPIFGMDVHRLMTATQYVAPLMAFNFG-----YSDNSTVYVFDN 61  
Db 108 LTAACSGFVF-----ALSTAEKFTIA--SGRFQKGLVIGSTLSKAVDWSRSTAVLFGD 159

Qy 62 GTVFVW----QWDHVYLGWEDKGS-----FTFOAA-----LHHDGRIV-- 96  
Db 160 GAGGVLEASQEHFLAELNSDGRSCLTYGHSLHSPDSQESADSLFKMDGRIVFD 219

Qy 97 FAYKEIPMSVPE 108  
Db 220 FAIRDVAKSIKO 231

RESULT 11  
S77723  
vitamin B12 receptor - Citrobacter freundii (fragment)  
C;Species: Citrobacter freundii  
C;Date: 24-Oct-1998 #sequence\_revision 24-Oct-1998 #text\_change 09-Jul-2004  
C;Accession: S77723  
R;Ward, R.J.; Glass, R.E.  
Mol. Microbiol. 16, 813-815, 1995  
A;Title: The 3'-terminal half of the btuB gene of Citrobacter freundii defines essential  
A;Reference number: S77723; MUID:96065709; PMID:7476175  
A;Accession: S77723  
A;Status: not compared with conceptual translation  
A;Molecule type: DNA  
A;Residues: 1-337 <WAR>  
A;Cross-references: UNIPROT:O52903  
C;Genetics:  
A;Gene: btuB  
C;Superfamily: vitamin B12 receptor; tonB-dependent receptor amino-terminal homology; to  
C;Keywords: membrane protein; vitamin B12 transport  
F;85-337/Domain: tonB-dependent receptor carboxyl-terminal homology <TNC>

Query Match 11.6%; Score 68; DB 2; Length 337;  
Best Local Similarity 20.7%; Pred. No. 13;  
Matches 23; Conservative 12; Mismatches 38; Indels 38; Gaps 2;

Qy 24 FMGDVHRLMTATQYVAPLMAFNFGYSDNSTVYVFDNGTVFVQWHD----- 71  
Db 1 FNGELIQSLVSS--YSHSKDYNPDYGRYDSSATLDEMKNQVWQNSIVVGHGNVGAG 59

Qy 72 -----VYLQGWEDKGSFTFOALHHDGRIVF 97  
Db 60 VDMQKQTTEPGYVTDGVDQRNTGLYLTGLQQLGDFTFEAAARDNDNSEF 110

RESULT 12

JH0289

class I histocompatibility antigen precursor (clone FLA-B9) - cat (fragment)  
C;Species: Felis silvestris catus (domestic cat)  
C;Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 09-Jul-2004  
C;Accession: JH0289  
R;Yuhki, N.; O'Brien, S.J.  
J. Exp. Med. 172, 621-630, 1990

A;Title: DNA recombination and natural selection pressure sustain genetic sequence diver  
A;Reference number: JH0288; MUID:90324882; PMID:1695669

A;Accession: JH0289

A;Molecule type: mRNA

A;Residues: 1-356 <YUH>

A;Cross-references: UNIPROT:Q95485; GB:U07672; NID:g467252; PIDN:AAA19462.1; PID:g467253

A;Experimental source: spleen

C;Superfamily: class I histocompatibility antigen; immunoglobulin homology

C;Keywords: transmembrane protein

F;1-18/Domain: signal sequence (fragment) #status predicted <SIG>

F;19-356/Product: class I histocompatibility antigen #status predicted <MAT>

F;19-108/Domain: alpha-1 <AL1>

F;109-200/Domain: alpha-2 <AL2>

F;201-292/Domain: alpha-3 <AL3>

F;214-279/Domain: immunoglobulin homology <IMM>

F;293-323/Domain: transmembrane #status predicted <TDO>

F;324-356/Domain: intracellular #status predicted <INT>

Query Match 11.5%; Score 67.5; DB 2; Length 356;  
Best Local Similarity 24.8%; Pred. No. 16;  
Matches 30; Conservative 16; Mismatches 40; Indels 35; Gaps 6;

Qy 10 HPLRQIATIG-----GFIFMGDVIHRLMTATQYV-----APLMAFNFP 48

Db 21 HSLRYFYTAVRPGGLGPRFIAGYV-----DDTQFVRFDSDAPNPREPRAPWVGVP 75

Qy 49 GYSDNSTVYVFDNGTVFVQWHDVYLGWEDK----GSFTFOALHHD-----GRIVFAYKE 101

Db 76 EYWDNRTRIYLDTAQIFRVSLENT--RGYVNSGSGSHNFQMYGCDIGPYGRLLRGYSQ 133

Qy 102 I 102

Db 134 M 134

RESULT 13

S18606

phosphoenolpyruvate carboxykinase (ATP) (EC 4.1.1.49) - Rhizobium sp.  
C;Species: Rhizobium sp.  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 27-Oct-2003  
C;Accession: S18606  
R;Osteras, M.; Finan, T.M.; Stanley, J.  
Mol. Gen. Genet. 230, 257-269, 1991

A;Title: Site-directed mutagenesis and DNA sequence of pckA of Rhizobium NGR234, encodin

A;Reference number: S18606; MUID:92079905; PMID:1720862

A;Accession: S18606

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-535 <OST>

A;Cross-references: EMBL:X63291

C;Superfamily: phosphoenolpyruvate carboxykinase [ATP]

C;Keywords: carbon-carbon lyase; carboxy-lyase; nucleotide binding; P-loop

F;234-241/Region: nucleotide-binding motif A (P-loop)

Query Match 11.5%; Score 67.5; DB 2; Length 535;  
Best Local Similarity 21.3%; Pred. No. 25;  
Matches 20; Conservative 12; Mismatches 35; Indels 27; Gaps 4;

Qy 17 IATGGTIFMGDVIHRLMTATQYVAP-----LMANFNPGYSDNSTVYVF----- 59

Db 186 VLIIGTSYAGEMKKSFTVLNLLPNKAVMDHCSANVGPA---GDTAIFPLGLSGTGKTT 242

Qy 60 ---DNGTVFVQWHDVYLGWEDKGSFTFOALH 90

Db 243 LSADPNRTLIGDDEH----GWSDKGVNFEGGCY 272

## RESULT 14

JC4553  
heme d1 synthesis protein nirF - Pseudomonas aeruginosa  
C:Species: Pseudomonas aeruginosa  
C:Date: 12-Mar-1996 #sequence\_revision 19-Apr-1996 #text\_change 09-Jul-2004  
C:Accession: JC4553; H83581  
R:Kawasaki, S.; Arai, H.; Igarashi, Y.; Kodama, T.  
Gene 167, 87-91, 1995  
A:Title: Sequencing and characterization of the downstream region of the genes encoding Y for biosynthesis of heme d1.  
A:Reference number: JC4552; MUID:96144254; PMID:8566817  
A:Accession: JC4553  
A:Molecule type: DNA  
A:Residues: 1-392 <KAW>  
A:Cross-references: UNIPROT:Q51480; DDBJ:D50473; NID:g1217594; PIDN:BAA09066.1; PID:g1217594  
A:Experimental source: RM31  
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Boman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A:Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen.  
A:Reference number: A82950; MUID:20437337; PMID:10984043  
A:Accession: H83581  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-392 <STO>  
A:Cross-references: GB:AE004488; GB:AE004091; NID:g9946372; PIDN:AAG03905.1; GSPDB:GN001488  
A:Experimental source: strain PAO1  
C:Genetics:  
A:Gene: nirF; PA0516  
C:Superfamily: Pseudomonas stutzeri heme d1 synthesis protein nirF

Query Match 11.4%; Score 67; DB 2; Length 392;  
Best Local Similarity 28.2%; Pred. No. 20;  
Matches 22; Conservative 10; Mismatches 30; Indels 16; Gaps 2;  
  
Qy 37 QYVAPLMANFPGYSDNSTV-----YFNGTVFVV---QMDHVLQGWEDK 80  
Db 134 ELVAEIPATRLPGQDRNSRVGLVDAPGQRFVSLFDSGEIWIADFSQGDTPHLTRFRDI 193  
  
Qy 81 GSFTFQAAALHHDGRIVFA 98  
Db 194 GKQPYDALISPDGRYYMA 211

## RESULT 15

B82510  
transporter, NadC family VCA0025 [imported] - Vibrio cholerae (strain N16961 serogroup O1)  
C:Species: Vibrio cholerae  
C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004  
C:Accession: B82510  
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, J.; R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.  
Nature 406, 477-483, 2000  
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.  
A:Reference number: A82035; MUID:20406833; PMID:10952301  
A:Accession: B82510  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-462 <HEI>  
A:Cross-references: UNIPROT:Q9KNE0; GB:AE004346; GB:AE003853; NID:g9657401; PIDN:AAF9593  
A:Experimental source: serogroup O1; strain N16961; biotype El Tor  
C:Genetics:  
A:Gene: VCA0025  
A:Map position: 2  
C:Superfamily: probable transporter MJ0672

Query Match 11.4%; Score 67; DB 2; Length 462;  
Best Local Similarity 23.9%; Pred. No. 24;  
Matches 17; Conservative 14; Mismatches 26; Indels 14; Gaps 2;

Qy 23 IFMGDVIRMLTATQYVAPLMANFPGYSDNSTVYFNGTVFVVQMDHVLQGWEDKGS 82  
Db 58 LMLTEALH--VTVTAILVPVMAVFGIFETQAAALNNFANSIIFLF-----LGG 103  
  
Qy 83 FTFOAALHHDG 93  
Db 104 FALAAAMHHQG 114

Search completed: January 28, 2005, 22:12:39  
Job time : 9.47923 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 28, 2005, 21:56:43 ; Search time 40.6279 Seconds  
(without alignments)  
816.164 Million cell updates/sec

Title: US-09-918-715-230

Perfect score: 2691

Sequence: 1 MRGELWLLVLVLRARALS.....YAEVPSGHEKGFMEAEQC 500

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.\*

- 1: /cgn2\_6/ptodata/1/iaa/5A.COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/iaa/5B.COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/iaa/6A.COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/iaa/6B.COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/iaa/PTUS.COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2185	81.2	431	4	US-09-912-935-36
2	1295	48.1	499	4	US-09-912-935-31
3	1295	48.1	529	4	US-09-912-935-28
4	1295	48.1	529	4	US-09-912-935-40
5	1276	47.4	425	4	US-09-912-935-35
6	1275.5	47.4	530	4	US-09-912-935-38
7	1176.5	43.7	392	4	US-09-764-325A-23
8	1176.5	43.7	392	4	US-09-764-325A-25
9	1176.5	43.7	392	4	US-09-912-935-23
10	1176.5	43.7	392	4	US-09-912-935-25
11	1055	39.2	449	4	US-09-912-935-34
12	115.5	4.3	1568	3	US-09-181-706-2
13	115.5	4.3	1568	3	US-09-458-791-2
14	115.5	4.3	1568	3	US-09-459-066-2
15	115.5	4.3	1568	3	US-09-459-065-2
16	97	3.6	712	4	US-08-543-681A-6132
17	95.5	3.5	3052	2	US-08-557-122A-26
18	95.5	3.5	3052	3	US-09-262-666-26
19	93.5	3.5	1977	4	US-09-976-594-757
20	93.5	3.5	1977	4	US-09-919-039-367
21	93	3.5	1085	1	US-08-431-080-28
22	93	3.5	1085	2	US-08-938-534-28
23	93	3.5	1085	3	US-09-345-294-28
24	92.5	3.4	518	4	US-09-816-248-17
25	92.5	3.4	1220	1	US-08-158-232-43
26	92.5	3.4	1220	2	US-08-611-928-43
27	92.5	3.4	1220	3	US-09-173-891-43

RESULT 1  
US-09-912-935-36  
; Sequence 36, Application US/09912935  
; Patent No. 6673904  
; GENERAL INFORMATION:  
; APPLICANT: Nishikawa, Mitsuo et al.  
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE  
; FILE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES  
; FILE REFERENCE: 32066/37483  
; CURRENT APPLICATION NUMBER: US/09/912.935  
; CURRENT FILING DATE: 2001-07-24  
; PRIOR APPLICATION NUMBER: PCT/US00/35260  
; PRIOR FILING DATE: 2000-12-23  
; NUMBER OF SEQ ID NOS: 53  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 36  
; LENGTH: 431  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-912-935-36

28	30.5	3.4	424	2	US-08-484-993B-18	Sequence 18, Appl
29	30.5	3.4	424	2	US-08-484-158B-18	Sequence 18, Appl
30	30.5	3.4	424	2	US-08-484-596A-18	Sequence 18, Appl
31	30.5	3.4	424	2	US-08-480-150A-18	Sequence 18, Appl
32	30.5	3.4	424	2	US-08-458-731-18	Sequence 18, Appl
33	30.5	3.4	424	2	US-08-149-223A-18	Sequence 18, Appl
34	89.5	3.3	424	6	5169835-6	Patent No. 5169835
35	89.5	3.3	446	4	US-09-252-991A-31114	Sequence 31114, A
36	89	3.3	517	4	US-09-248-796A-14652	Sequence 14652, A
37	89	3.3	595	2	US-08-232-087A-2	Sequence 2, Appl
38	89	3.3	595	3	US-09-006-353A-9	Sequence 9, Appl
39	89	3.3	595	4	US-09-573-986-9	Sequence 9, Appl
40	88.5	3.3	15281	2	US-08-471-119A-2	Sequence 2, Appl
41	88	3.3	490	4	US-09-461-325-250	Sequence 250, App
42	88	3.3	490	4	US-09-461-325-518	Sequence 518, App
43	88	3.3	490	4	US-10-012-542-250	Sequence 250, App
44	88	3.3	490	4	US-10-012-542-518	Sequence 518, App
45	88	3.3	490	4	US-10-115-123-250	Sequence 250, App

ALIGNMENTS

Query Match	81.2%	Score	2185;	DB	4;	Length	431;
Best Local Similarity	95.2%	Pred. No.	1.3e-209;				
Matches	416;	Conservative	0;	Mismatches	7;	Indels	14;
Gaps	3;						
Qy	72	LAMDTLPDNRTRVVEDNHSYVSRLYGSPSPHSGRELWVDVAENRSQVKIHTILSNTHRQ	131				
Db	1	LAMDTLPDNRTRVVEDNHSYVSRLYGSPSPHSGRELWVDVAENRSQVKIHTILSNTHRQ	60				
Qy	132	ASRVLSDFPFYCHPLROITATGGIFMGDVTHRLMTATQYVAPLMAFNPCYSDNST	191				
Db	61	ASRVLSDFPFYCHPLROITATGGIFMGDVTHRLMTATQYVAPLMAFNPCYSDNST	120				
Qy	192	VYVFDNGTGVVQWDHVLQGWEDKGSFTFOALHHDGRIVFAYKEIPMSVPEISSSQHP	251				
Db	121	VYVFDNGTGVVQWDHVLQGWEDKGSFTFOALHHDGRIVFAYKEIPMSVPEISSSQHP	180				
Qy	252	VKTGLSDAFMLNPSDPVPSRRRSIFEXHRIELDPKSVTSMASVEFTPLPTCLQHRSCD	311				
Db	181	VKTGLSDAFMLNPSDPVPSRRRSIFEXHRIELDPKSVTSMASVEFTPLPTCLQHRSCD	240				
Qy	312	ACWSSDLTFNCSCWCHVLQRCSSGFDYRQEW-WDYGCAQAEGRMCEDFQD-----ED	363				
Db	241	ACWSSDLTFNCSCWCHVLQRCSSGFDYRQEW-WDYGCAQAEGRMCEDFQD-----QDVRGLPGMRT	294				
Qy	364	HDASPDTSFSPDGDLTITSSSLFIDSLTETDDTKLNPYAGGDLQNNLSPKTKGTGVH	423				
Db	295	TTASPDTSFSPDGDLTITSSSLFIDSLTETDDTKLNPYAGGDLQNNLSPKTKGTGVH	354				
Qy	424	LGTIVGIVLAVLLVAAILAGIVINGHPTNNAALFFIERRPHHPWAMKFRSHDPHSTYAE	483				

Db 355 LGTIVGIVLAVLLVAAIILAGIYINGHTSNAALFFIERRPHHPAMKFRSHPDHSTYAE 414  
Qy 484 VEPSGHEKEGFMEAEQC 500  
Db 415 VEPSGHEKEGFMEAEQC 431

RESULT 2

US-09-912-935-31  
; Sequence 31, Application US/09912935  
; Patent No. 6673904  
; GENERAL INFORMATION:  
; APPLICANT: Nishikawa, Mitsuo et al.  
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE  
; FILE REFERENCE: 32066/37483  
; CURRENT APPLICATION NUMBER: US/09/912,935  
; CURRENT FILING DATE: 2001-07-24  
; PRIOR APPLICATION NUMBER: PCT/US00/35260  
; PRIOR FILING DATE: 2000-12-23  
; NUMBER OF SEQ ID NOS: 53  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 31  
; LENGTH: 499  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-912-935-31

Query Match 48.1%; Score 1295; DB 4; Length 499;  
Best Local Similarity 57.3%; Pred. No. 1.6e-120;  
Matches 250; Conservative 72; Mismatches 166; Indels 8; Gaps 5;  
Qy 72 LAMDTLPDNRTRVVED-NHSYVYVRLYGPSEPHSRELVDVAEANRSQVKIHTILSNTHR 130  
Db 65 LLLDDGQDNNTQIEEDTDHNYIISRIYGPSDSASRDVLWNIDQMEKDKVKIHGILSNTHR 124  
Qy 131 QASRVLSFDPFPGHPLRQIATIGGFIEMGDVHRLMTATQYVAPLMAFNFPYSDNS 190  
Db 125 QAAVNLSFDPFPGHPLRQIATIGGFIEMGDVHRLMTATQYVAPLMAFNFPYSDNS 184  
Qy 191 TVVYFDNGTVFVQWHDVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPEISSQH 250  
Db 185 TVRFDNGTALVQWHDVHLQDNYNLGSFTFQAALLMDGRIFGYKEIPVLVTQISSTNH 244  
Qy 251 PVKTGLSDAFMILNPSDPVPSRRSIFEYHRIELDPKVTSMGSAVEFTPLPTCLQHRSC 310  
Db 245 PVKVGLSDAFVVRHRIQIIPNVRRTIYEVHRLQMSKITNISAVEMTPLPTCLQFNRC 304  
Qy 311 DACWSSDLTNCSCWCHVLRQCSGFDRIYRQEMDYGCAQEAEGRMCEDFQDEHDSASPD 370  
Db 305 GPCVSSQIGFNCSCWCKLQRCSSGFDRIYRQEMDYGCAQEAEGRMCEDEPTVETSSRTTT 364  
Qy 371 T-SFSPYDGLTTTS---SSLFIDSLTTEDDTKLNYPAGDGLQ--NNLSPKTKGTVPVHL 424  
Db 365 TIGATTQFVLVTTTRAVTSQFPTSLPTEDDTKIALHLKXNGASTDSDAAEKGKGTILHA 424  
Qy 425 GTTIVGIVLAVLLVAAIILAGIYINGHTSNAALFFIERRPHHPAMKFRSHPDHSTYAEV 484  
Db 425 GLIVGILILVIVATALLVTVVYHHTPSAASIFFIERRPSPWPMKFRGSGHPAYAEV 484  
Qy 485 EPSGHEKEGFMEAEQC 500  
Db 485 EPVGE-EKEGFIVSEQC 499

RESULT 3

US-09-912-935-28  
; Sequence 28, Application US/09912935  
; Patent No. 6673904  
; GENERAL INFORMATION:  
; APPLICANT: Nishikawa, Mitsuo et al.  
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE

; TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES  
; FILE REFERENCE: 32066/37483  
; CURRENT APPLICATION NUMBER: US/09/912,935  
; CURRENT FILING DATE: 2001-07-24  
; PRIOR APPLICATION NUMBER: PCT/US00/35260  
; PRIOR FILING DATE: 2000-12-23  
; NUMBER OF SEQ ID NOS: 53  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 28  
; LENGTH: 529  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-912-935-28

Query Match 48.1%; Score 1295; DB 4; Length 529;  
Best Local Similarity 57.3%; Pred. No. 1.7e-120;  
Matches 250; Conservative 72; Mismatches 106; Indels 8; Gaps 5;  
Qy 72 LAMDTLPDNRTRVVED-NHSYVYVRLYGPSEPHSRELVDVAEANRSQVKIHTILSNTHR 130  
Db 95 LLLDDGQDNNTQIEEDTDHNYIISRIYGPSDSASRDVLWNIDQMEKDKVKIHGILSNTHR 154  
Qy 131 QASRVLSFDPFPGHPLRQIATIGGFIEMGDVHRLMTATQYVAPLMAFNFPYSDNS 190  
Db 155 QAAVNLSFDPFPGHPLRQIATIGGFIEMGDVHRLMTATQYVAPLMAFNFPYSDNS 214  
Qy 191 TVVYFDNGTVFVQWHDVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPEISSQH 250  
Db 215 TVRFDNGTALVQWHDVHLQDNYNLGSFTFQAALLMDGRIFGYKEIPVLVTQISSTNH 274  
Qy 251 PVKTGLSDAFMILNPSDPVPSRRSIFEYHRIELDPKVTSMGSAVEFTPLPTCLQHRSC 310  
Db 275 PVKVGLSDAFVVRHRIQIIPNVRRTIYEVHRLQMSKITNISAVEMTPLPTCLQFNRC 334  
Qy 311 DACWSSDLTNCSCWCHVLRQCSGFDRIYRQEMDYGCAQEAEGRMCEDFQDEHDSASPD 370  
Db 335 GPCVSSQIGFNCSCWCKLQRCSSGFDRIYRQEMDYGCAQEAEGRMCEDEPTVETSSRTTT 394  
Qy 371 T-SFSPYDGLTTTS---SSLFIDSLTTEDDTKLNYPAGDGLQ--NNLSPKTKGTVPVHL 424  
Db 395 TIGATTQFVLVTTTRAVTSQFPTSLPTEDDTKIALHLKXNGASTDSDAAEKGKGTILHA 454  
Qy 425 GTTIVGIVLAVLLVAAIILAGIYINGHTSNAALFFIERRPHHPAMKFRSHPDHSTYAEV 484  
Db 455 GLIVGILILVIVATALLVTVVYHHTPSAASIFFIERRPSPWPMKFRGSGHPAYAEV 514  
Qy 485 EPSGHEKEGFMEAEQC 500  
Db 515 EPVGE-EKEGFIVSEQC 529

RESULT 4

US-09-912-935-40  
; Sequence 40, Application US/09912935  
; Patent No. 6673904  
; GENERAL INFORMATION:  
; APPLICANT: Nishikawa, Mitsuo et al.  
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE  
; FILE REFERENCE: 32066/37483  
; CURRENT APPLICATION NUMBER: US/09/912,935  
; CURRENT FILING DATE: 2001-07-24  
; PRIOR APPLICATION NUMBER: PCT/US00/35260  
; PRIOR FILING DATE: 2000-12-23  
; NUMBER OF SEQ ID NOS: 53  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 40  
; LENGTH: 529  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-912-935-40

Query Match 48.1%; Score 1295; DB 4; Length 529;







Qy	310	CDACMSSDLTFCNSCHVLQRCSSGFDYRQE-----WMDYGAQAEGRMCEDFQ-----D 367
Db	461	CSECLTA-TDPHCWGCHSLQRCCTQDCVHSENLENWLDI-----SSGAKCCKPKIQIRSS 515
Qy	362	EDHDSASPDTSFSP 375
Db	516	KETITVMVGSFSP 529
<p>RESULT 13</p> <p>US-09-458-791-2</p> <p>; Sequence 2, Application US/09458791</p> <p>; Patent No. 6174689</p> <p>; GENERAL INFORMATION:</p> <p>; APPLICANT: Spriggs, Melanie</p> <p>; TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN</p> <p>; RECEPTOR DNA AND POLYPEPTIDES</p> <p>; NUMBER OF SEQUENCES: 10</p> <p>; CORRESPONDENCE ADDRESS:</p> <p>; ADDRESSEE: Janis C. Henry</p> <p>; STREET: 51 University St.</p> <p>; CITY: Seattle</p> <p>; STATE: WA</p> <p>; COUNTRY: US</p> <p>; ZIP: 98101</p> <p>; COMPUTER READABLE FORM:</p> <p>; MEDIUM TYPE: Floppy disk</p> <p>; OPERATING SYSTEM: MS-DOS/Windows 95</p> <p>; SOFTWARE: Word for Windows 95, 7.0a</p> <p>; CURRENT APPLICATION DATA:</p> <p>; APPLICATION NUMBER: US/09/458,791</p> <p>; FILING DATE: 10-Dec-1999</p> <p>; CLASSIFICATION: &lt;Unknown&gt;</p> <p>; PRIOR APPLICATION DATA:</p> <p>; APPLICATION NUMBER: 08/958,598</p> <p>; FILING DATE: 28-OCT-1997</p> <p>; ATTORNEY/AGENT INFORMATION:</p> <p>; NAME: Henry, Janis C</p> <p>; REGISTRATION NUMBER: 34,347</p> <p>; REFERENCE/DOCKET NUMBER: 2631</p> <p>; TELECOMMUNICATION INFORMATION:</p> <p>; TELEPHONE: (206)470-4189</p> <p>; TELEFAX: (206)233-0644</p> <p>; INFORMATION FOR SEQ ID NO: 2:</p> <p>; SEQUENCE CHARACTERISTICS:</p> <p>; LENGTH: 1569 amino acids</p> <p>; TYPE: amino acid</p> <p>; TOPOLOGY: linear</p> <p>; MOLECULE TYPE: protein</p> <p>; SEQUENCE DESCRIPTION: SEQ ID NO: 2:</p> <p>US-09-458-791-2</p>		
Qy	39	GTVGRNRRARESPGHVSEPDRT---QLSQDLGGGTLMADTLPDNRTRVVEDNHNHYVS 94
Db	256	GAATGHPSPMAR-----IAQSTEVLFQGGASLDCGHG-----PDGR-----R 292
Qy	95	RLYGPSEPHSRLWDV--AEANRSQVKIHTI-----LSNTHROASRVVLSF----- 139
Db	293	LLLSLSSVLVEALDVWAGVFSAAAGEGQERRSPPTTALCLFRMSEIQARAKRVSWDFKTAES 352
Qy	140	-----DPFYGHPRLRITTIATGGTFIMGDVIHRMLTATQYVAPLMANFNPGYSDNSTVYV 194
Db	353	HCKEGDQPERVQPIASSTL-----IHSDLTSV-YGTVM-----NRTVLP 391
Qy	195	FONGTVFVQWDHVLYLQGWEDKGSFTFOAALHHDGRI--VFAYKEIPMSVPEI---SSSQ 249
Db	392	LGTTG-----DKQLLKVLIGENLTNCCEVIYEIKEE 422
Qy	250	HPVKTGLSDAFMLNPSPDVPSPRRRSIPFYHRIELDPKVTSMASVAFETPLPTCLOHRS 309
Db	423	TPV-----FYKLVDP-----VKNIIY-----LTAGKEVRIRIVANCXKHS 460
<p>Query Match 4.3%; Score 115.5; DB 3; Length 1568;</p> <p>Best Local Similarity 20.6%; Pred. No. 0.086;</p> <p>Matches 77; Conservative 42; Mismatches 118; Indels 137; Gaps 20;</p>		
Qy	39	GTVGRNRRARESPGHVSEPDRT---QLSQDLGGGTLMADTLPDNRTRVVEDNHNHYVS 94
Db	256	GAATGHPSPMAR-----IAQSTEVLFQGGASLDCGHG-----PDGR-----R 292
Qy	95	RLYGPSEPHSRLWDV--AEANRSQVKIHTI-----LSNTHROASRVVLSF----- 139
Db	293	LLLSLSSVLVEALDVWAGVFSAAAGEGQERRSPPTTALCLFRMSEIQARAKRVSWDFKTAES 352
Qy	140	-----DPFYGHPRLRITTIATGGTFIMGDVIHRMLTATQYVAPLMANFNPGYSDNSTVYV 194
Db	353	HCKEGDQPERVQPIASSTL-----IHSDLTSV-YGTVM-----NRTVLP 391
Qy	195	FONGTVFVQWDHVLYLQGWEDKGSFTFOAALHHDGRI--VFAYKEIPMSVPEI---SSSQ 249
Db	392	LGTTG-----DKQLLKVLIGENLTNCCEVIYEIKEE 422
Qy	250	HPVKTGLSDAFMLNPSPDVPSPRRRSIPFYHRIELDPKVTSMASVAFETPLPTCLOHRS 309
Db	423	TPV-----FYKLVDP-----VKNIIY-----LTAGKEVRIRIVANCXKHS 460

QY 250 HPVTKGLSDAFMILNPSDPVPSRRRSIFFEYHRIELDPSKVTSMASAVEFTPLPTCLOHRS 309  
DB 423 TPV-----FYKLVDP-----VKNIYY-----LTAGKEVRRIRVANCNKHS 460  
QY 310 CDACMSDLTFCNSCHVLQRCSSGFDYRQE-----WMDYCAQAEAGRMCEDFQ-----D 361  
DB 461 CSECLTA-TDPCGCHSLQRCCTQGCDCVHSENLENWLDI-----SSGAKKCPKIQIRSS 515  
QY 362 EDHDSASPDTSFSP 375  
DB 516 KEKTTVTMVGFSFP 529  
RESULT 14  
US-09-459-066-2  
; Sequence 2, Application US/09459066  
; Patent No. 6187909  
; GENERAL INFORMATION:  
; APPLICANT: Spriggs, Melanie  
; TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN  
; TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Janis C. Henry  
; STREET: 51 University St.  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: US  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: MS-DOS/Windows 95  
; SOFTWARE: Word for Windows 95, 7.0a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/459,066  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/958,598  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Henry, Janis C  
; REGISTRATION NUMBER: 34,347  
; REFERENCE/DOCKET NUMBER: 2631  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206)470-4189  
; TELEFAX: (206)233-0644  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1568 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-459-066-2  
Query Match 4.3%; Score 115.5; DB 3; Length 1568;  
Best Local Similarity 20.6%; Pred. No. 0.086;  
Matches 77; Conservative 42; Mismatches 118; Indels 137; Gaps 20;  
QY 39 GTVRGWNRRAESPGHVSEPDRT-----QLSQDLGGGTLMADTLPDNRTRVVEDNHSYVS 94  
DB 256 GAATGWPSMAR-----IAQSTEVLFQQAASLDCGHG-----PDGR-----R 292  
QY 95 RLYGPSEPHSRELWVDV--AEANRSQVKIHTI-----LSNTHROASRVVLSF----- 139  
DB 293 LLLSSLSVEALDWAGVFSAAAGGQERRSPPTTALCLFRMSEIQARAKRVSDFKTAES 352  
QY 140 -----DPPFYGHPLQRIQTATGGFIEMGDVTHRLMTATQVAPLMAFNPCYSDNSTVY 194  
DB 353 HCKEGDQPERVQPIASTL-----IHSDLTSV-YGVVM-----NRTLVF 391  
QY 195 FDNGTVFVQWDHYVLQGWEDKGSFTTQAAALHHDGRI--VFAYKEIPMSVPEI-----SSSQ 249

DB 392 LGTG-----DQOLLKVLGNLTNSNCEVIYIEKBE 422  
QY 250 HPVTKGLSDAFMILNPSDPVPSRRRSIFFEYHRIELDPSKVTSMASAVEFTPLPTCLOHRS 309  
DB 423 TPV-----FYKLVDP-----VKNIYY-----LTAGKEVRRIRVANCNKHS 460  
QY 310 CDACMSDLTFCNSCHVLQRCSSGFDYRQE-----WMDYCAQAEAGRMCEDFQ-----D 361  
DB 461 CSECLTA-TDPCGCHSLQRCCTQGCDCVHSENLENWLDI-----SSGAKKCPKIQIRSS 515  
QY 362 EDHDSASPDTSFSP 375  
DB 516 KEKTTVTMVGFSFP 529  
RESULT 15  
US-09-459-065-2  
; Sequence 2, Application US/09459065  
; Patent No. 6562949  
; GENERAL INFORMATION:  
; APPLICANT: Spriggs, Melanie  
; TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN  
; TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Janis C. Henry  
; STREET: 51 University St.  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: US  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: MS-DOS/Windows 95  
; SOFTWARE: Word for Windows 95, 7.0a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/459,065  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/958,598  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Henry, Janis C  
; REGISTRATION NUMBER: 34,347  
; REFERENCE/DOCKET NUMBER: 2631  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206)470-4189  
; TELEFAX: (206)233-0644  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1568 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-459-065-2  
Query Match 4.3%; Score 115.5; DB 4; Length 1568;  
Best Local Similarity 20.6%; Pred. No. 0.086;  
Matches 77; Conservative 42; Mismatches 118; Indels 137; Gaps 20;  
QY 39 GTVRGWNRRAESPGHVSEPDRT-----QLSQDLGGGTLMADTLPDNRTRVVEDNHSYVS 94  
DB 256 GAATGWPSMAR-----IAQSTEVLFQQAASLDCGHG-----PDGR-----R 292  
QY 95 RLYGPSEPHSRELWVDV--AEANRSQVKIHTI-----LSNTHROASRVVLSF----- 139  
DB 293 LLLSSLSVEALDWAGVFSAAAGGQERRSPPTTALCLFRMSEIQARAKRVSDFKTAES 352  
QY 140 -----DPPFYGHPLQRIQTATGGFIEMGDVTHRLMTATQVAPLMAFNPCYSDNSTVY 194

Db 353 HKEGQDQPERVQPIASSTL-----IHSDLTsv-YGTvVM-----NRTVLF 391  
Qy 195 FDNGTVFVQWDHVYVLOGWEDKSGFTFOALHHDGRI--VFAYKEIPMSVPEI---SSSQ 249  
Db 392 LGTG-----DQQLKVLGENLTSNCPEVIYEIKEE 422  
Qy 250 HPVKTGLSDAFMILNPSPDVPESRRRSIFEYHRIELDPFSKVTSMsAVEFTPLPTCLOHRS 309  
Db 423 TPV-----FYKLVDP-----VKNIYY-----LTAGKEVRRIRVANCNKHS 460  
Qy 310 CDACMSSDLTFNCsWCHVLQRCSSGFDRYOE----WMDYGCAQEAEGRMCEQF----D 361  
Db 461 CSECLTA-TDPHCGWCHSLQRCCTFGDCVHSENLENWLDI-----SSGAKKCPKIQIRSS 515  
Qy 362 EDHDSASPDTSFSP 375  
Db 516 KEKTTVTMTVGSFSP 529

Search completed: January 28, 2005, 22:14:18  
Job time : 42.8779 secs



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OM protein - protein search, using sw model

Run on: January 28, 2005, 21:55:58 ; Search time 34.626 Seconds  
(without alignments)  
1389.370 Million cell updates/sec

Title: US-09-918-715-230  
Perfect score: 2891  
Sequence: 1 MRGELMLLVLVREARALS.....YAEVPSGHEKGFMEAEQC 500  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	611	22.7	476	2 T19786	hypothetical prote
2	126	4.7	1161	1 S31213	nidogen precursor
3	115.5	4.3	1568	2 T09074	semaphorin recepto
4	103.5	3.8	979	2 C86446	probable cellulose
5	101.5	3.8	743	2 T09173	EH domain protein
6	101	3.8	733	2 E86345	hypothetical prote
7	100	3.7	535	2 S18606	phosphoenolpyruvat
8	99	3.7	1133	2 T12529	hypothetical prote
9	98	3.6	345	2 T16074	hypothetical prote
10	98	3.6	1502	2 S45429	probable membrane
11	97	3.6	708	2 T83196	NEDD-4 ORF - mouse
12	96.5	3.6	397	2 S33415	corticosteroid-bin
13	96.5	3.6	679	2 T19703	hypothetical prote
14	95.5	3.5	399	1 S71480	homeotic protein H
15	95.5	3.5	887	2 S70642	ubiquitin ligase N
16	95.5	3.5	2120	2 T30243	alpha tectorin - c
17	94	3.5	774	2 JC7265	nephrysin (EC 3.4
18	93.5	3.5	979	1 JC2349	protein-tyrosine-p
19	93.5	3.5	996	2 T48721	PTP 35 protein - m
20	93.5	3.5	1977	2 S54771	sodium channel alp
21	93	3.5	491	2 AG3506	phosphoenolpyruvat
22	93	3.5	1085	2 S53352	IFH1 protein - yea
23	92.5	3.4	441	2 JC7653	pectate lyase (EC
24	92.5	3.4	852	2 T85041	probable receptor
25	91.5	3.4	614	2 A98241	hypothetical prote
26	91.5	3.4	614	2 P86088	hypothetical prote
27	91.5	3.4	810	1 P2WMBB	2a protein - broad
28	91.5	3.4	1042	2 A57534	mucin 5AC (clone L
29	91	3.4	633	2 S47144	mating type A prot

30	91	3.4	1175	2 S51005	protein-tyrosine-p
31	90.5	3.4	332	2 JN0067	pregnancy-specific
32	90.5	3.4	424	2 S70399	zona pellucida gly
33	90.5	3.4	4848	2 T30289	pristinamycin I sy
34	90	3.3	561	2 AD2581	phosphoenolpyruvat
35	90	3.3	561	2 B97363	phosphoenolpyruvat
36	90	3.3	798	2 T25104	hypothetical prote
37	90	3.3	1176	2 I58345	protein tyrosine p
38	90	3.3	1179	2 T05673	hypothetical prote
39	90	3.3	1189	2 T51491	hypothetical prote
40	90	3.3	1621	2 T30200	protein-tyrosine k
41	90	3.3	2825	2 T14271	Doc4 protein, stre
42	89.5	3.3	424	2 A34595	pregnancy-specific
43	89.5	3.3	1376	2 G00043	osteonidogen - hum
44	89.5	3.3	1762	2 T03222	probable polyketid
45	89.5	3.3	1840	1 CHRTM1	sodium channel pro

ALIGNMENTS

RESULT 1

T19786  
hypothetical protein C36E8.3 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T19786  
R;Wilkinson, J.; Barlow, K.  
submitted to the EMBL Data Library, August 1994  
A;Reference number: Z19177  
A;Accession: T19786  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-476 <WIL>  
A;Cross-references: UNIPROT:Q18500; EMBL:Z35597; PIDN:CAA84646.1; GSPDB:GNO0021; CESP:C3  
A;Experimental source: clone C36E8  
C;Genetics:  
A;Gene: CESP:C36E8.3  
A;Map position: 3  
A;Introns: 23/1; 101/3; 152/3; 206/3; 235/1; 255/3; 320/1; 445/2  
C;Superfamily: Caenorhabditis elegans hypothetical protein C36E8.3

Query Match	22.7%	Score 611;	DB 2;	Length 476;
Best Local Similarity	34.2%	Pred. No. 5.6e-42;		
Matches 149;	Conservative	65;	Mismatches 160;	Indels 62; Gaps 15;
Qy	46	RRARESPGVSEPDRTQLS-----QDLGGGTFLAMDTLPDNKRTRVEDNHSYVVSRLYGPS	100	
Db	62	RTAAAP-----IPRSLASQDEDEEDIDPATATIP--PDVEVKNDMDHQYQAEFTVGD	115	
Qy	101	EPHSRELWVDVAENRSQVKI-----HTILSNTHROASRVVLSFDFPFYGHPLRQITATG	156	
Db	116	GETLKKYWINVEQFMKKPKAVGNTSHELLSQSYRRVAVGARLQPKFPFYGHKMSNLIATG	175	
Qy	157	GFIFMGDVIRHMLTATQYVAPLMAFNPGVSDNSTVYFNGTVFVYQWHDVHYLQGHEDK	216	
Db	176	GFYIGDHSNHLAATQYIAPLMAFNFT-YLNNSNIVYADGGELFVYVWRNVQLKDKDE	234	
Qy	217	GSTTFQAAHLHGDRIYPAKKEIPMSVPEISSQHPVKTGLSDAFMILN--PSPDVPESRR	274	
Db	235	HSFTFQILHKGNDIVFYIKDVPYDINISDANHPVKLGISDAYMFKHNLHQAAP---K	291	
Qy	275	RSIFEVHRIELDPKSVTSMASVEFTPLPTCLQHRSCDACMSSDLT-FNCSCWCHVLR---	330	
Db	292	RVIVEVHRIEIAAKIVSNVWILKAQPTCISPDCTCTNATLPHENCLWCHAKKSHGG	351	
Qy	331	--CS--SGFPRYQEWMDYCAQAEGRMCE-DFQEDDHDSAS--PDTSFSPYDGLTTTS	384	
Db	352	PFCTDEAGLHRRRHQHWFEQNGYQSRKALYCDADDEDEYDEEDYPKSQLPMNGGH---	408	
Qy	385	SSLFIDSLTTEDDTKLNPKYAGGDLQNNLSPKTKGTPVHLGTIVGIVLVAALLAAILAG	444	
Db	409	LPLDADQMKTKDTTSDSDSEWKGHKKEEPK-----GG	442	

Qy 445 IYINGHP--TSNAALF 458  
Db 443 VATTAPVGTSSQAATF 458

RESULT 2  
S31213  
nidogen precursor - sea squirt (Halocynthia roretzi)  
N;Alternate names: entactin  
C;Species: Halocynthia roretzi  
C;Date: 30-Sep-1993 #sequence\_revision 27-Feb-1997 #text\_change 09-Jul-2004  
C;Accession: S31213  
R;Nakae, H.; Sugano, M.; Ishimori, Y.; Endo, T.; Obinata, T.  
Eur. J. Biochem. 213, 11-19, 1993  
A;Title: Ascidian entactin/nidogen. Implication of evolution by shuffling two kinds of c  
A;Reference number: S31213; MUID:93238676; PMID:8477687  
A;Accession: S31213  
A;Molecule type: mRNA  
A;Residues: 1-1161 <NAK>  
A;Cross-references: UNIPROT:Q04901; EMBL:D14038; NID:g217363; PIDN:BA03127.1; PID:g2173  
C;Superfamily: Ascidian nidogen; EGF homology; LDL receptor WYTD-containing repeat homol  
C;Keywords: basement membrane; collagen binding; disulfide bond; duplication; extracellu  
F;1-20/Domain: signal sequence #status predicted <SIG>  
F;21-1161/Product: nidogen #status predicted <MAT>  
F;274-306/Domain: EGF homology <EGI>  
F;560-574/Region: 3-residue repeats (R-P-V)  
F;603-673/Domain: thyroglobulin type I repeat homology <THY1>  
F;686-748/Domain: thyroglobulin type I repeat homology <THY2>  
F;752-819/Domain: thyroglobulin type I repeat homology <THY3>  
F;900-943/Domain: LDL receptor WYTD-containing repeat homology <YW1>  
F;944-986/Domain: LDL receptor WYTD-containing repeat homology <YW2>  
F;987-1031/Domain: LDL receptor WYTD-containing repeat homology <YW3>  
F;1032-1075/Domain: LDL receptor WYTD-containing repeat homology <YW4>  
F;1076-1114/Domain: LDL receptor WYTD-containing repeat homology <YW4>  
F;1129-1158/Domain: EGF homology <EG2>  
F;107,334,360,484/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 4.7%; Score 126; DB 1; Length 1161;  
Best Local Similarity 23.5%; Pred. No. 0.094;  
Matches 64; Conservative 34; Mismatches 88; Indels 86; Gaps 12;

Qy 137 LSPDFPFVGHPLROITATGGFIEM-----GDVTHRLMTATQYVAPLMAN----- 181  
Db 47 LSMPIVFYDKYDSVHTDGFITLNVGADTDGEVL-----LAPFMSDLDTLSG 97

Qy 182 --FNPGYSDNSTVYV-----PDNGTVFVQWDHYVLOGWEDKGSFTFQAA 224  
Db 98 DIFPREHKDNATIRANTDVREAFIETAGDFNAGSVFVVTWQKVSASREDGVTFITQCI 157

Qy 225 LHHGRIVFA---YKEIPMSVPEIS-----SSQHPVKYGLSDA-----FWILNPSP-----DV 269  
Db 158 VATDGAATFAIFLYPDGLAVGENAVKVRNEVTARAGFNDGGRQLEILSADLLGGDN 217

Qy 270 PESRRRSFFVHRTLDPSKVTSMASVEFTPLCTLOHRSACDMSDLTFNCSCWCHVLQ 329  
Db 218 AGSQGQWIFQGGWFWNDEASKSE-----KH-----HWK 249

Qy 330 RCSSGFDYRQEW-MDYGCAQAE-GRMCEDF 359  
Db 250 TRQSGFQVSEVFNEDFNIDLEACGTPCSDF 281

RESULT 3  
T09074  
semaphorin receptor VESPR - human  
C;Species: Homo sapiens (man)  
C;Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004  
C;Accession: T09074  
R;Comeau, M.R.; Johnson, R.; DuBoise, R.F.; Petersen, M.; Gearing, P.; van den Bos, T.; F  
Immunity 8, 473-482, 1998  
A;Title: A poxvirus-encoded semaphorin induces cytokine production from monocytes and b  
A;Reference number: 216555; MUID:98246049; PMID:9586637

A;Accession: T09074  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-1568 <COM>  
A;Cross-references: UNIPROT:O60486; EMBL:AF030339; NID:g3176761; PIDN:AAC18823.1; PID:g3  
A;Experimental source: tissue type foreskin; cell type fibroblast  
C;Genetics:  
A;Gene: VESPR  
C;Keywords: receptor; signal transduction

Query Match 4.3%; Score 115.5; DB 2; Length 1568;  
Best Local Similarity 20.6%; Pred. No. 1;  
Matches 77; Conservative 42; Mismatches 118; Indels 137; Gaps 20;

Qy 39 GTVRGNNRRARSPGHVSEPDRT-----QLSQDLGGGTFLAMDTLPDNRTRVVEDNHSYVS 94  
Db 256 GAATGWPSMAR-----IAQSTEVLFQQAASLDCGHG-----PDGR-----R 292

Qy 95 RLYGPSPHRSRELWVDV--AEANRSQVKIHTI-----LSNTHROASRWLSF----- 139  
Db 293 LLLSSSLVEALDVWAGVFAAEGGQRRSPPTTALCLFRMSEIQARAKRVSWDFKTAES 352

Qy 140 -----DPPFYGHPLRQITATGGFIEMGDVHRLMTATQYVAPLMANFPCYSDNSTVYV 194  
Db 353 HCKEGDQPERVQPIASSTL-----IHSDLTSV-YGTVM-----NRTVLF 391

Qy 195 FDNGTVPVQWDHYVLOGWEDKGSFTFOAALHHDGRI--VPAYKEIPMSVPEI-----SSSQ 249  
Db 392 LGTG-----DGQLLKVLGENTLSTNCPEVIYEKEE 422

Qy 250 HPVKYGLSDAFMILNPSPDPVPESSRRRSIFVHRIELDPSPKVTSMASVEFTPLCTLOHRS 309  
Db 423 TPV-----FYKLVPDP-----VKNIYY-----LTAGEVRRIRVANCNKHKS 460

Qy 310 CDACMSDLTFNCSCWCHVLQRCSSGFDYRQE-----WMDYGCQAQAEGRMCEDFQ-----D 361  
Db 461 CSECLTA-TDPHCGWCHSLQRCITQCGDVHSENLENWLDI-----SSGAKKPKIQLIRSS 515

Qy 362 EDHDSASPDTSFSP 375  
Db 516 KEKTTVTVMVGSFSP 529

RESULT 4  
C86446  
probable cellulose synthase catalytic subunit [imported] - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C;Accession: C86446  
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federapfel, N.A.; Kaul, S.; White, O.; Alonso,  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;  
ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A;Reference number: A86141; MUID:21016719; PMID:11130712  
A;Accession: C86446  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-979 <STO>  
A;Cross-references: UNIPROT:Q9FVR3; GB:AB005172; NID:g10801364; PIDN:AAG23436.1; GSPDB:G  
C;Genetics:  
A;Map position: 1

Query Match 3.8%; Score 103.5; DB 2; Length 979;  
Best Local Similarity 21.2%; Pred. No. 5.2;  
Matches 87; Conservative 48; Mismatches 167; Indels 109; Gaps 19;

Qy 4 ELWLLVLVLRRAARALSPQAGHDEGPGGWAAKGTVRGWNNRRAARESPGHVSEPDRTQL 63

Db 342 EKWKHKVKEEDQIKPRPAL---VAPKATWMSDGT--HWPGTWAVSGPHHSRGDHSV 396  
Qy 64 SQDL-----GGTLAMD-----TLPDNRTRVEDNHSYVSRLYGSPSEHSR 105  
Db 397 IQVLLDPGDPVKGKGEGRALDLLEGVDIRLP-----MLVYSREKRGYDHNK 446  
Qy 106 ELWVDVAEANKRSQVHIHTILNTHROASRVVLSFDPFPYGHPLRQITATGGFIFMGDVI 165  
Db 447 K-----AGAMNALVRASAIMSN-----GPFILNLCDDHYVNSRAF---RDGICFWMDDH 493  
Qy 166 HRLMTATQY-----VAPLMAFNPCYSD-----NSTVYV-F 195  
Db 494 GDRVSYVQFPQRFEGIDFSDRYANKNTVFFDINLRALDGIQGMVYGTGCLFRETALYGF 553  
Qy 196 DNGTVFVQVVDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPMSV---PEISSQHP- 251  
Db 554 NPPDVFE-----EPPSGSCFP-----LTKRSATVASEPEYTYDDEDR 595  
Qy 252 -----VKTGLSDAFMILNPSDPVPSRRRSIFEYH--RIELDPKVT-SMSAVEFTPLPT 303  
Db 596 FDIGLIRKQFGSSMLVN-SVKVAEFEGRPLATVHSSRLGRPPGSLTGSRRKPLDFATVNE 654  
Qy 304 CLQHRSCDACMSSDLTFCNSWCH--VLQRCSSGDFRQEWMDYGCQAQEA 352  
Db 655 AVNVISCWYEDKTEWGFNVGVIYGSVTEDVVTGFRMEHKGWRSPYCVTEPD 705  
RESULT 5  
T09173  
EH domain protein Repel - mouse  
N;Alternate names: RalBP1-associated EH domain protein Repel1  
C;Species: Mus musculus (house mouse)  
C;Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004  
C;Accession: T09173  
J.Yamaguchi, A.; Urano, T.; Goi, T.; Feig, L.A.  
R. Biol. Chem. 272, 31230-31234, 1997  
A;Title: An eps homology (EH) domain protein that binds to the ral-GTPase target, RalBP1  
A;Reference number: 216602; MUID:98059900; PMID:9395447  
A;Accession: T09173  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-743 <YAM>  
A;Cross-references: UNIPROT:O54916; EMBL:AF031939; NID:g2677842; PIDN:AAB94736.1; PID:g2677842  
A;Experimental source: cell line: C2C12; tissue type: muscle  
C;Genetics:  
A;Gene: repel  
C;Keywords: signal transduction  
Query Match 3.8%; Score 101.5; DB 2; Length 743;  
Best Local Similarity 18.3%; Pred. No. 5.1;  
Matches 91; Conservative 63; Mismatches 166; Indels 177; Gaps 23;  
Qy 19 LSPQPGAGH-DEPGSGWAAK-----GTVRGWNRARESPGHV 55  
Db 78 IPPPPGRGVKGGSHDAVQPRSAEQCEPAPVSPQQSPPTSPHTWRKHSRPGSGN 137  
Qy 56 SEPRTQLSQ-----DLGGTLDWDTLPDNRTRVEDNHSYVSRLYGSPSEHSRELW 109  
Db 138 SERPLTGGPWPSPFGAQSSAGDAV-----WSGSPPPPPQDNW 179  
Qy 110 DVAE-----ANRSQVXIHTLS-NTHQASRVVLSPDFFPYGHPLRQITAT 155  
Db 180 SFADTPPTSALLTWPASVQDQTTVTRVASAATANEIRQSSSYEDPW-----KITDE- 232  
Qy 156 GGFIFMGDVIHRLMTATQY--VAPLMAFNPCYSDNSTVYVVDNGTVFVQVMDHYV-LQG 212  
Db 233 -----ORQYVNVQFTIQPLNGFIPG---SAAKEFFTKSKLPILSHLWELSD 279  
Qy 213 WEDKGSFT---FOALHHDGRIVFAYK---EIPMSVPEISSQHPVKTGLSDAFMILNPS 266  
Db 280 FDKDGLATLDEFCFAFH-----LVVARXNGYDLPEKLPE-----SLMPKLIDLEDS 325

Qy 267 PDVPESRRRSIFEYHRIELDPKSVTSMASAVEFTPLPTCLOHRSCDACMSSDLTFCNSWCH 326  
Db 326 ADVGEQPGVGSYSGSPAPSPSPSPSPSL-----NQTWPE 361  
Qy 327 VLQRCSSGDFRYQEWMDYGCQAQEAECRMCEDEQEDHDSASPDTS----- 372  
Db 362 LNOS-----SEQWETFS-ERSSSQTLTQF-DSNIAFPADPTALVHPVPIRMTFSKI 411  
Qy 373 -----FSPYDGLITTTSSSLFIDSLTDEDTKLNP-----YAGDGLQNLNLS 414  
Db 412 HMQEMELKPTSSDHTNPTPLVKPDLSEENKINSSVKPNTVGDYSSSDSPSPD-- 469  
Qy 415 PKTKGTPV-----HLGT 426  
Db 470 PEQTGSSVTRQSRHSGT 486  
RESULT 6  
E86345  
hypothetical protein FlGf4.9 - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C;Accession: E86345  
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federapiel, N.A.; Kaul, S.; White, O.; Alonso,  
ansen, N.F.; Chung, M.K.; Conn, L.; Conway, A.B.; Huizar, L.  
Nature 408, 816-820, 2000  
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A;Reference number: A86141; MUID:21016719; PMID:11130712  
A;Accession: E86345  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-733 <STO>  
A;Cross-references: UNIPROT:Q9LMN7; GB:AE005172; NID:g8920637; PIDN:AAF81359.1; GSPDB:GN  
C;Genetics:  
A;Map position: 1  
C;Superfamily: Arabidopsis probable serine/threonine-specific protein kinase PRO25; prot  
Query Match 3.8%; Score 101; DB 2; Length 733;  
Best Local Similarity 24.1%; Pred. No. 5.5;  
Matches 59; Conservative 24; Mismatches 72; Indels 90; Gaps 13;  
Qy 257 SDAFMIILNPSDPVPSRRRSI-----FEVHRIELDPKSVTSMASAVE-FTPLPTCL 305  
Db 139 STGCMSLCTDTPPPNSKCNVGCCTREVSIPLDISHRIETQPSRFENMTSVEHFN----- 193  
Qy 306 QHRSCD-ACMSSDLTFNCS-----WCHVLQRC-----SS 333  
Db 194 -----CSVAFFVEDGMFNFSLEDLKOLNVRTRPVLWDNIGNQTCQVGVNRNCGNST 249  
Qy 334 GFDRYQEWMDYGCQAQEAECRM-----CEDFQD---EDHDSASPD-----SF-SPY 376  
Db 250 CFDSRCKGYNCKLQCGFDGPNVLSDCQDINECTRIHNCSDDTSTCENTIGSFHCQCP 309  
Qy 377 DGLITTTSSSLFIDSLTDEDTKLNPYAGDGLQNLNLSPTKGTG-TPVHLGTIVIGIVLAVL 435  
Db 310 GSDLNTTMSK-IDTPKEE-----PKYLGWTTVLLGTTGTLIGLILL 349  
Qy 436 LVAAL 440  
Db 350 TISYI 354  
RESULT 7  
S18606  
phosphoenolpyruvate carboxykinase (ATP) (EC 4.1.1.49) - Rhizobium sp.  
C;Species: Rhizobium sp.  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 27-Oct-2003







F;54-167/Domain: protein kinase C C2 region homology <KC2>

F;246-283/Domain: WW repeat homology <WW1>

F;402-439/Domain: WW repeat homology <WW2>

F;459-496/Domain: WW repeat homology <WW3>

F;555-881/Domain: ubiquitin-protein ligase homology <UB1>

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Query Match          3.5%; Score 95.5; DB 2; Length 887;
Best Local Similarity 19.2%; Pred. No. 20;
Matches 93; Conservative 55; Mismatches 155; Indels 181; Gaps 25;

Qy 14 EAARALSP-----QPGAG-----HDEGPG-----SGWAKGTVRG-----WNRR 47
Db 218 DQAELEPGVVLQPDADATHLQHPPEPSPLPPGWERQDVLGRTYYVNHESRTQWKRP 277
Qy 48 ARES-----PCHVSEPDRTQLSQDLGGGTLAMDTLPDNRTR-----VVEDNH 89
Db 278 SPEDDLTDDENGDIQLQAHGAFTTRQISEVDG-----PDHESPENWEIVREDEN 329
Qy 90 SYVYSR-LYGPSEPHSRELWVDVAENRSQVKIHTILSNTHRQASRVVLSFDFPFYGHPL 148
Db 330 TIYSGQAVQSPSGHP-DVQVRLAE-----ELDTRLT-----MYGNPA 366
Qy 149 RQITATCGFTFMGDVIHRLMTATQYVAPLM-----ANENPGY-----SDNSTVVYFDNGTV 200
Db 367 TSQPVTSNHSRGSSQTCIFEEQPTLPVLPTSSGLPPGWEKQDDRGYSYYVDHNSK 426
Qy 201 FVQWDHYVYLQ-----GWEDKGSFTFQAALHHDGRIVF 233
Db 427 -TTTWSKPTMQDDPRSKIPAHLRGKTPVDSNDLGLPLPGWEER-----THTDGRVFF 477
Qy 234 AYKEIPMSVPEISSQHPVKTGLSDAFMLNPSDVPESR-RRSIFPYHRIELDPKVT 292
Db 478 INHNKKTQWEDPRMQNVAITG-----PAEPYSRDYKRYEFFFFRKLKKQ---- 522
Qy 293 MSAVEFTPLPTCLOHRSCDACMSDLTFNCSCWCHVLCRCSSGDFRYRQEWMDYCAQBAE 352
Db 523 -----TDIPNKFENK-----LRRAILEDSEYRR-IMGVGRADFLK 556
Qy 353 GRMCEDFQDE---DHDSASPD-----TSFSPYDGDLTSTSSSLFIDSLTTEDDT-KLN 401
Db 557 ARLWIEFDGEGKGLDYGVAWEWFFLISKEMENPYG-----LFEYSATEDNYTLQIN 608
Qy 402 PYAG 405
Db 609 PNSG 612
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Search completed: January 28, 2005, 22:12:46  
Job time : 36.626 secs

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Db 61 TQLSODLGGGTAMDTLPDNRTRVVDNHSYVSRLYGSPSPHRELWVDVAEANRSQVK 120
Qy 121 IHTILSNTHROASRVLSFDFPFYGHPLRQITATGGFIFMGDVIHRMLTATQVAPLMA 180
Db 121 IHTILSNTHROASRVLSFDFPFYGHPLRQITATGGFIFMGDVIHRMLTATQVAPLMA 180
Qy 181 NFNPYSDNSTVYVFDNGTVFVQWDHVYLGWEDKGSFTFQAALHHDGRIVPAYKEIPM 240
Db 181 NFNPYSDNSTVYVFDNGTVFVQWDHVYLGWEDKGSFTFQAALHHDGRIVPAYKEIPM 240
Qy 241 SVPEISSSQHPVKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKVTSMASAVEFTP 300
Db 241 SVPEISSSQHPVKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKVTSMASAVEFTP 300
Qy 301 LPTCLOHRSCDACMSSDLTFNCWCHVLQRCSSGFDYRQWMDYGAQBAEGRMCEDFQ 360
Db 301 LPTCLOHRSCDACMSSDLTFNCWCHVLQRCSSGFDYRQWMDYGAQBAEGRMCEDFQ 360
Qy 361 DEDHDSASPDTSFSPYDGLTFTTSSSLFIDSLTTEDDTKLNYPAGGDLQNNLSPKTKGT 420
Db 361 DEDHDSASPDTSFSPYDGLTFTTSSSLFIDSLTTEDDTKLNYPAGGDLQNNLSPKTKGT 420
Qy 421 PVHLGTTIGVILVALLVAAILAGIYINGHPTSNAALFFIERRPHWPAMKFRSHPDHST 480
Db 421 PVHLGTTIGVILVALLVAAILAGIYINGHPTSNAALFFIERRPHWPAMKFRSHPDHST 480
Qy 481 YAEVPSGHEKEGFMPEARQC 500
Db 481 YAEVPSGHEKEGFMPEARQC 500

RESULT 2
US-10-435-696-79
; Sequence 79, Application US/10435696
; Publication No. US20040018525A1
; GENERAL INFORMATION:
; APPLICANT: Wirtz, Ralph
; APPLICANT: Munes, Marc
; APPLICANT: Kallabis, Harald
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE PREDICTION, DIAGNOSIS, PROGNOSIS
; TITLE OF INVENTION: PREVENTION AND TREATMENT OF MALIGNANT NEOPLASIA
; FILE REFERENCE: Lea 36 108
; CURRENT APPLICATION NUMBER: US/10/435,696
; PRIOR FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: EP03003112.4
; PRIOR FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: EP02010291.9
; PRIOR FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 314
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 79
; LENGTH: 500
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-435-696-79

Query Match 100.0%; Score 2691; DB 15; Length 500;
Best Local Similarity 100.0%; Pred. No. 4.9e-249;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRGELWLLVLVLRARALSPQAGHDEGPGSGWAAKGTVRGWNRRARESPGHVSPDR 60
Db 1 MRGELWLLVLVLRARALSPQAGHDEGPGSGWAAKGTVRGWNRRARESPGHVSPDR 60
Qy 61 TQLSODLGGGTAMDTLPDNRTRVVDNHSYVSRLYGSPSPHRELWVDVAEANRSQVK 120
Db 61 TQLSODLGGGTAMDTLPDNRTRVVDNHSYVSRLYGSPSPHRELWVDVAEANRSQVK 120
Qy 121 IHTILSNTHROASRVLSFDFPFYGHPLRQITATGGFIFMGDVIHRMLTATQVAPLMA 180
Db 121 IHTILSNTHROASRVLSFDFPFYGHPLRQITATGGFIFMGDVIHRMLTATQVAPLMA 180
Qy 181 NFNPYSDNSTVYVFDNGTVFVQWDHVYLGWEDKGSFTFQAALHHDGRIVPAYKEIPM 240
Db 181 NFNPYSDNSTVYVFDNGTVFVQWDHVYLGWEDKGSFTFQAALHHDGRIVPAYKEIPM 240
Qy 241 SVPEISSSQHPVKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKVTSMASAVEFTP 300
Db 241 SVPEISSSQHPVKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKVTSMASAVEFTP 300
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Db 181 NFNPYSDNSTVYVFDNGTVFVQWDHVYLGWEDKGSFTFQAALHHDGRIVPAYKEIPM 240
Qy 241 SVPEISSSQHPVKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKVTSMASAVEFTP 300
Db 241 SVPEISSSQHPVKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKVTSMASAVEFTP 300
Qy 301 LPTCLOHRSCDACMSSDLTFNCWCHVLQRCSSGFDYRQWMDYGAQBAEGRMCEDFQ 360
Db 301 LPTCLOHRSCDACMSSDLTFNCWCHVLQRCSSGFDYRQWMDYGAQBAEGRMCEDFQ 360
Qy 361 DEDHDSASPDTSFSPYDGLTFTTSSSLFIDSLTTEDDTKLNYPAGGDLQNNLSPKTKGT 420
Db 361 DEDHDSASPDTSFSPYDGLTFTTSSSLFIDSLTTEDDTKLNYPAGGDLQNNLSPKTKGT 420
Qy 421 PVHLGTTIGVILVALLVAAILAGIYINGHPTSNAALFFIERRPHWPAMKFRSHPDHST 480
Db 421 PVHLGTTIGVILVALLVAAILAGIYINGHPTSNAALFFIERRPHWPAMKFRSHPDHST 480
Qy 481 YAEVPSGHEKEGFMPEARQC 500
Db 481 YAEVPSGHEKEGFMPEARQC 500

RESULT 3
US-10-474-794-230
; Sequence 230, Application US/10474794
; Publication No. US20040213793A1
; GENERAL INFORMATION:
; APPLICANT: Carson-Walter, Eleanor
; APPLICANT: St. Croix, Brad
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00179
; CURRENT APPLICATION NUMBER: US/10/474,794
; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 60/308,829
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 359
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 230
; LENGTH: 500
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-474-794-230

Query Match 100.0%; Score 2691; DB 17; Length 500;
Best Local Similarity 100.0%; Pred. No. 4.9e-249;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRGELWLLVLVLRARALSPQAGHDEGPGSGWAAKGTVRGWNRRARESPGHVSPDR 60
Db 1 MRGELWLLVLVLRARALSPQAGHDEGPGSGWAAKGTVRGWNRRARESPGHVSPDR 60
Qy 61 TQLSODLGGGTAMDTLPDNRTRVVDNHSYVSRLYGSPSPHRELWVDVAEANRSQVK 120
Db 61 TQLSODLGGGTAMDTLPDNRTRVVDNHSYVSRLYGSPSPHRELWVDVAEANRSQVK 120
Qy 121 IHTILSNTHROASRVLSFDFPFYGHPLRQITATGGFIFMGDVIHRMLTATQVAPLMA 180
Db 121 IHTILSNTHROASRVLSFDFPFYGHPLRQITATGGFIFMGDVIHRMLTATQVAPLMA 180
Qy 181 NFNPYSDNSTVYVFDNGTVFVQWDHVYLGWEDKGSFTFQAALHHDGRIVPAYKEIPM 240
Db 181 NFNPYSDNSTVYVFDNGTVFVQWDHVYLGWEDKGSFTFQAALHHDGRIVPAYKEIPM 240
Qy 241 SVPEISSSQHPVKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKVTSMASAVEFTP 300
Db 241 SVPEISSSQHPVKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKVTSMASAVEFTP 300
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Db 503 MRGELWLLVLVLRRAARALSPQAGHDEGPGSGWAAGKTVRGWNRRAESPCHVSBPDR 562
Qy 61 TQLSQDLGGGTAMDITLPDNRTRVEDNHSYVSRLYGPPSPHRELVWDVAEANRSQVK 120
Db 563 TQLSQDLGGGTAMDITLPDNRTRVEDNHSYVSRLYGPPSPHRELVWDVAEANRSQVK 622
Qy 121 IHTILSNTHQASRVLSFDFFPGHPLRQITITATGGFIFMGDVIHRMLTATQYVAPLMA 180
Db 623 IHTILSNTHQASRVLSFDFFPGHPLRQITITATGGFIFMGDVIHRMLTATQYVAPLMA 682
Qy 181 NFNPYSDNSTVYFNGTVFVQWDHVVYLGWEDKGSFTFQAALHHDGRIVFAYKEIPM 240
Db 683 NFNPYSDNSTVYFNGTVFVQWDHVVYLGWEDKGSFTFQAALHHDGRIVFAYKEIPM 742
Qy 241 SVPEISSQHPVKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKSVTSMASVEFTP 300
Db 743 SVPEISSQHPVKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKSVTSMASVEFTP 802
Qy 301 LPTCLQHRSCDACMSSDLTFNCSSCHVLRQCSGFDYRQEWMDYGCQAQEAEGRMCDFFQ 360
Db 803 LPTCLQHRSCDACMSSDLTFNCSSCHVLRQCSGFDYRQEWMDYGCQAQEAEGRMCDFFQ 862
Qy 361 DEDHDSASPTSFSPYDGLTTTSSSLFIDSLTTEDDTKLNYPYAGDGLQNNLSPKTKGT 420
Db 863 DEDHDSASPTSFSPYDGLTTTSSSLFIDSLTTEDDTKLNYPYAGDGLQNNLSPKTKGT 922
Qy 421 PVHLGTTIVGIVLAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPDHST 480
Db 923 PVHLGTTIVGIVLAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPDHST 982
Qy 481 YAEVPSGHEKEGFMEAEQC 500
Db 983 YAEVPSGHEKEGFMEAEQC 1002

RESULT 6
US-10-474-794-179
; Sequence 179, Application US/10474794
; Publication No. US20040213793A1
; GENERAL INFORMATION:
; APPLICANT: Carson-Walter, Eleanor
; APPLICANT: St. Croix, Brad
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00179
; CURRENT APPLICATION NUMBER: US/10/474,794
; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 60/308,829
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 359
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 179
; LENGTH: 1002
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-474-794-179

Query Match 100.0%; Score 2691; DB 17; Length 1002;
Best Local Similarity 100.0%; Pred. No. 1.4e-248;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRGELWLLVLVLRRAARALSPQAGHDEGPGSGWAAGKTVRGWNRRAESPCHVSBPDR 60
Db 503 MRGELWLLVLVLRRAARALSPQAGHDEGPGSGWAAGKTVRGWNRRAESPCHVSBPDR 562
Qy 61 TQLSQDLGGGTAMDITLPDNRTRVEDNHSYVSRLYGPPSPHRELVWDVAEANRSQVK 120
Db 563 TQLSQDLGGGTAMDITLPDNRTRVEDNHSYVSRLYGPPSPHRELVWDVAEANRSQVK 622
Qy 121 IHTILSNTHQASRVLSFDFFPGHPLRQITITATGGFIFMGDVIHRMLTATQYVAPLMA 180
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Db 623 IHTILSNTHQASRVLSFDFFPGHPLRQITITATGGFIFMGDVIHRMLTATQYVAPLMA 682
Qy 181 NFNPYSDNSTVYFNGTVFVQWDHVVYLGWEDKGSFTFQAALHHDGRIVFAYKEIPM 240
Db 683 NFNPYSDNSTVYFNGTVFVQWDHVVYLGWEDKGSFTFQAALHHDGRIVFAYKEIPM 742
Qy 241 SVPEISSQHPVKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKSVTSMASVEFTP 300
Db 743 SVPEISSQHPVKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKSVTSMASVEFTP 802
Qy 301 LPTCLQHRSCDACMSSDLTFNCSSCHVLRQCSGFDYRQEWMDYGCQAQEAEGRMCDFFQ 360
Db 803 LPTCLQHRSCDACMSSDLTFNCSSCHVLRQCSGFDYRQEWMDYGCQAQEAEGRMCDFFQ 862
Qy 361 DEDHDSASPTSFSPYDGLTTTSSSLFIDSLTTEDDTKLNYPYAGDGLQNNLSPKTKGT 420
Db 863 DEDHDSASPTSFSPYDGLTTTSSSLFIDSLTTEDDTKLNYPYAGDGLQNNLSPKTKGT 922
Qy 421 PVHLGTTIVGIVLAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPDHST 480
Db 923 PVHLGTTIVGIVLAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPDHST 982
Qy 481 YAEVPSGHEKEGFMEAEQC 500
Db 983 YAEVPSGHEKEGFMEAEQC 1002

RESULT 7
US-10-357-819-4
; Sequence 4, Application US/10357819
; Publication No. US20040259774A1
; GENERAL INFORMATION:
; APPLICANT: Alvarez, Enrique
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gangolli, Baha A.
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Gorman, Linda
; APPLICANT: Guo, Xiaojia
; APPLICANT: Ji, Weizhen
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Li, Li
; APPLICANT: Miller, Charles E.
; APPLICANT: Padigaru, Muraidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Rastelli, Luca
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-538A
; CURRENT APPLICATION NUMBER: US/10/357,819
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 09/584,411
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 09/783,436
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 10/085,198
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 60/353,301
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 60/355,099
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: 60/356,424
; PRIOR FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: 60/358,239
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: 60/358,608
; PRIOR FILING DATE: 2002-02-21
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;; PRIOR APPLICATION NUMBER: 60/359,367  
;; PRIOR FILING DATE: 2002-02-25  
;; Remaining Prior Application data removed - See File Wrapper or PALM.  
;; NUMBER OF SEQ ID NOS: 142  
;; SOFTWARE: CuraseqList version 0.1  
;; SEQ ID NO 4  
;; LENGTH: 488  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-10-357-819-4

Query Match 96.7%; Score 2602; DB 17; Length 488;  
Best Local Similarity 97.4%; Pred. No. 1.7e-240;  
Matches 487; Conservative 1; Mismatches 0; Indels 12; Gaps 1;

Qy 1 MRGELWLLVLRREARALSPQAGHDEGPGSGWAAKGTVRGNRRARESPGHVSEPD 60  
Db 1 MRGELWLLVLRREARALSPQAGHDEGPGSGWAAKGTVRGNRRARESPGHVSEPD 60

Qy 61 TQLSQDLGGGTFLAMDTLPDNRTRVVDNHSYVSRLYGPPSEPHSRELWVDVAEANRSQVK 120  
Db 61 TQLSQDLGGGTFLAMDTLPDNRTRVVDNHSYVSRLYGPPSEPHSRELWVDVAEANRSQVK 120

Qy 121 IHTILSNTHROASRVLSFDPFPFYGHPLRQITTIATGGFIEMGDVIHMLTATQVAPLMA 180  
Db 121 IHTILSNTHROASRVLSFDPFPFYGHPLRQITTIATGGFIEMGDVIHMLTATQVAPLMA 180

Qy 181 NFNPYSDNSTVYFDNGTVFVQWDHVLQGWEDKGSFTFOAALHHDGRIVPAYKEIPM 240  
Db 181 NFNPYSDNSTVYFDNGTVFVQWDHVLQGWEDKGSFTFOAALHHDGRIVPAYKEIPM 240

Qy 241 SVPEISSQHPVKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKVTSMASAVEFTP 300  
Db 241 SVPEISSQHPVKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKVTSMASAVEFTP 300

Qy 301 LPTCLQRSACDMSDLTFNCSCWCHVLRQCSGFDRIYQEW-MDYCAQAEAGRMCEDF 359  
Db 301 LPTCLQRSACDMSDLTFNCSCWCHVLRQCSGFDRIYQEW-MDYCAQAEAGRMCEDF 359

Qy 361 DEDHDSASPTSFSPYDGLTTTSSSLFIDSLTTEDDTKLNYPAGGGLQNNLSPKTKGT 420  
Db 361 DEDHDSASPTSFSPYDGLTTTSSSLFIDSLTTEDDTKLNYPAGGGLQNNLSPKTKGT 420

Qy 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAIFFIERRPHHPAMKFRSHPDHST 480  
Db 409 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAIFFIERRPHHPAMKFRSHPNHST 468

Qy 481 YAEVEPSGHEKEGFMFAEQ 500  
Db 469 YAEVEPSGHEKEGFMFAEQ 488

RESULT 8  
US-10-156-487A-5  
; Sequence 5, Application US/10156487A  
; Publication No. US20030092025A1  
; GENERAL INFORMATION:  
; APPLICANT: Juan, Todd  
; APPLICANT: Bass, Michael B.  
; APPLICANT: Olinet, John  
; TITLE OF INVENTION: Tumor Endothelial Marker 7a Molecules and Uses Thereof  
; FILE REFERENCE: 01-072-A  
; CURRENT APPLICATION NUMBER: US/10/156,487A  
; CURRENT FILING DATE: 2002-09-10  
; PRIOR APPLICATION NUMBER: 60/293,852  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 502  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-156-487A-5

Query Match 95.4%; Score 2566; DB 14; Length 502;  
Best Local Similarity 95.9%; Pred. No. 5e-237;  
Matches 487; Conservative 0; Mismatches 7; Indels 14; Gaps 3;

Qy 1 MRGELWLLVLRREARALSPQAGHDEGPGSGWAAKGTVRGNRRARESPGHVSEPD 60  
Db 1 MRGELWLLVLRREARALSPQAGHDEGPGSGWAAKGTVRGNRRARESPGHVSEPD 60

Qy 61 TQLSQDLGGGTFLAMDTLPDNRTRVVDNHSYVSRLYGPPSEPHSRELWVDVAEANRSQVK 120  
Db 61 TQLSQDLGGGTFLAMDTLPDNRTRVVDNHSYVSRLYGPPSEPHSRELWVDVAEANRSQVK 120

Qy 121 IHTILSNTHROASRVLSFDPFPFYGHPLRQITTIATGGFIEMGDVIHMLTATQVAPLMA 180  
Db 121 IHTILSNTHROASRVLSFDPFPFYGHPLRQITTIATGGFIEMGDVIHMLTATQVAPLMA 180

Qy 181 NFNPYSDNSTVYFDNGTVFVQWDHVLQGWEDKGSFTFOAALHHDGRIVPAYKEIPM 240  
Db 181 NFNPYSDNSTVYFDNGTVFVQWDHVLQGWEDKGSFTFOAALHHDGRIVPAYKEIPM 240

Qy 241 SVPEISSQHPVKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKVTSMASAVEFTP 300  
Db 241 SVPEISSQHPVKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKVTSMASAVEFTP 300

Qy 301 LPTCLQRSACDMSDLTFNCSCWCHVLRQCSGFDRIYQEW-MDYCAQAEAGRMCEDF 359  
Db 301 LPTCLQRSACDMSDLTFNCSCWCHVLRQCSGFDRIYQEW-MDYCAQAEAGRMCEDF 359

Qy 360 QD-----EDHDSASPTSFSPYDGLTTTSSSLFIDSLTTEDDTKLNYPAGGGLQNN 412  
Db 355 QDVRGLPGMRTTTSASPTSFSPYDGLTTTSSSLFIDSLTTEDDTKLNYPAGGGLQNN 414

Qy 413 LSPKTKTTPVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAIFFIERRPHHPAMK 472  
Db 415 LSPKTKTTPVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAIFFIERRPHHPAMK 474

Qy 473 RSHPDHSTYAEVPSGHEKEGFMFAEQ 500  
Db 475 RSHPDHSTYAEVPSGHEKEGFMFAEQ 502

RESULT 9  
US-09-918-715-192  
; Sequence 192, Application US/09918715  
; Publication No. US20030017157A1  
; GENERAL INFORMATION:  
; APPLICANT: Brad St. Croix  
; APPLICANT: Bert Vogelstein  
; APPLICANT: Kenneth Kinzler  
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS  
; FILE REFERENCE: 1107.00134  
; CURRENT APPLICATION NUMBER: US/09/918,715  
; CURRENT FILING DATE: 2001-08-01  
; PRIOR APPLICATION NUMBER: 60/222,599  
; PRIOR FILING DATE: 2000-08-02  
; PRIOR APPLICATION NUMBER: 60/224,360  
; PRIOR FILING DATE: 2000-08-11  
; PRIOR APPLICATION NUMBER: 60/282,850  
; PRIOR FILING DATE: 2000-04-11  
; NUMBER OF SEQ ID NOS: 358  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 192  
; LENGTH: 500  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-918-715-192

Query Match 82.1%; Score 2209; DB 10; Length 500;  
Best Local Similarity 81.6%; Pred. No. 9.6e-203;  
Matches 409; Conservative 46; Mismatches 44; Indels 2; Gaps 2;

Qy 1 MRGELWLLVLRREARALSPQAGHDEGPGSGWAAKGTVRGNRRARESPGHVSEPD 59

Db 1 MRAQLWLLQLLLRGAARALSPATPAGHNEQDSAWTAKTRQGSRRPRESPAQVLKPG 60  
Qy 60 RTQLSQDLGGGTGLAMDTLPDNRTRVVDNHNHYYVSRVYGPSEPHSRRLWVDVAEANSQV 119  
Db 61 KTQLSQDLGGGSLAIDTLPDNRTRVVDNHNHYYVSRVYGPGEKQSQDLWVDLAVANRSHV 120  
Qy 120 KIHTILSNTHROASRVVLSFDFFPGYHPLRQITATGGFIFMGDVIHRMLTATQYVAPLM 179  
Db 121 KIHRILSSSHRQASRVVLSFDFFPGYHPLRQITATGGFIFMGDMLHRMLTATQYVAPLM 180  
Qy 180 ANFNPGYSDNSTVYVFQWQDHVYLQGWEDKGSFTFOAALHHDGRIVPAYKEIP 239  
Db 181 ANFNPGYSDNSTVAYFDNGTVFVQWQDHVYLQDREDRGSFTFOAALHHDGRIVFGYKEIP 240  
Qy 240 MSVPEISSOHVPKVTGLSDAFMILNPSDPVPESSRRSIFEYHRIELDPKVTSMASAVEFT 299  
Db 241 MAVLDISSAQHPKAGLSDAFMIILNSPEVPSQRRTIFEYHRVELDSSKITTTSAVEFT 300  
Qy 300 PLPTCLOHRSQCDACMSSDLTFCNSCHVLCRCSSGFDYRQEWMDYCAQAEAGMCEDF 359  
Db 301 PLPTCLOHQSCDTCVSSNLTFNCSCVLCRCSSGFDYRQEWMLTYCAQAEAGKTCEDF 360  
Qy 360 QDEHDGASPDTSFSPYDGLTUTSSSLFIDSLTTEDDTKLNPYAGDGLQNNLSPKTKG 419  
Db 361 QDDSHYSASPDSSFPFNGD-STTSSSLFIDSLTTEDDTKLNPYAGDGLPDHSSPKSG 419  
Qy 420 TPVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPWPKFRSHPDHS 479  
Db 420 PPVHLGTIVGIVLAVLLVAAILAGIYISGHPNSNAALFFIERRPHHPWPKFHNPHNS 479  
Qy 480 TYAEVPSGHEKGFMEAEQC 500  
Db 480 TYTEVEPSGHEKGFVEAEQC 500

RESULT 10

US-09-918-715-297  
; Sequence 297, Application US/09918715  
; Publication No. US20030017157A1  
; GENERAL INFORMATION:  
; APPLICANT: Brad St. Croix  
; APPLICANT: Bert Vogelstein  
; APPLICANT: Kenneth Kinzler  
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS  
; FILE REFERENCE: 1107.00134  
; CURRENT APPLICATION NUMBER: US/09/918.715  
; CURRENT FILING DATE: 2001-08-01  
; PRIOR APPLICATION NUMBER: 60/222,599  
; PRIOR FILING DATE: 2000-08-02  
; PRIOR APPLICATION NUMBER: 60/224,360  
; PRIOR FILING DATE: 2000-08-11  
; PRIOR APPLICATION NUMBER: 60/282,850  
; PRIOR FILING DATE: 2000-04-11  
; NUMBER OF SEQ ID NOS: 358  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 297  
; LENGTH: 500  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-918-715-297

Query Match 82.1%; Score 2209; DB 10; Length 500;  
Best Local Similarity 81.6%; Pred. No. 9.6e-203;  
Matches 409; Conservative 46; Mismatches 44; Indels 2; Gaps 2;  
Qy 1 MRGELWLL-VLVLRGAARALSPQAGHDEGPGSGWAAGTGVRCWNRRAESPCHVSEPD 59  
Db 1 MRAQLWLLQLLLRGAARALSPATPAGHNEQDSAWTAKTRQGSRRPRESPAQVLKPG 60  
Qy 60 RTQLSQDLGGGTGLAMDTLPDNRTRVVDNHNHYYVSRVYGPSEPHSRRLWVDVAEANSQV 119  
Db 61 KTQLSQDLGGGSLAIDTLPDNRTRVVDNHNHYYVSRVYGPGEKQSQDLWVDLAVANRSHV 120

Qy 120 KIHTILSNTHROASRVVLSFDFFPGYHPLRQITATGGFIFMGDVIHRMLTATQYVAPLM 179  
Db 121 KIHRILSSSHRQASRVVLSFDFFPGYHPLRQITATGGFIFMGDMLHRMLTATQYVAPLM 180  
Qy 180 ANFNPGYSDNSTVYVFQWQDHVYLQGWEDKGSFTFOAALHHDGRIVPAYKEIP 239  
Db 181 ANFNPGYSDNSTVAYFDNGTVFVQWQDHVYLQDREDRGSFTFOAALHHDGRIVFGYKEIP 240  
Qy 240 MSVPEISSOHVPKVTGLSDAFMILNPSDPVPESSRRSIFEYHRIELDPKVTSMASAVEFT 299  
Db 241 MAVLDISSAQHPKAGLSDAFMIILNSPEVPSQRRTIFEYHRVELDSSKITTTSAVEFT 300  
Qy 300 PLPTCLOHRSQCDACMSSDLTFCNSCHVLCRCSSGFDYRQEWMDYCAQAEAGMCEDF 359  
Db 301 PLPTCLOHQSCDTCVSSNLTFNCSCVLCRCSSGFDYRQEWMLTYCAQAEAGKTCEDF 360  
Qy 360 QDEHDGASPDTSFSPYDGLTUTSSSLFIDSLTTEDDTKLNPYAGDGLQNNLSPKTKG 419  
Db 361 QDDSHYSASPDSSFPFNGD-STTSSSLFIDSLTTEDDTKLNPYAGDGLPDHSSPKSG 419  
Qy 420 TPVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPWPKFRSHPDHS 479  
Db 420 PPVHLGTIVGIVLAVLLVAAILAGIYISGHPNSNAALFFIERRPHHPWPKFHNPHNS 479  
Qy 480 TYAEVPSGHEKGFMEAEQC 500  
Db 480 TYTEVEPSGHEKGFVEAEQC 500

RESULT 11  
US-10-156-487A-6  
; Sequence 6, Application US/10156487A  
; Publication No. US20030092025A1  
; GENERAL INFORMATION:  
; APPLICANT: Juan, Todd  
; APPLICANT: Bass, Michael B.  
; APPLICANT: Oliner, John  
; TITLE OF INVENTION: Tumor Endothelial Marker 7a Molecules and Uses Thereof  
; FILE REFERENCE: 01-072-A  
; CURRENT APPLICATION NUMBER: US/10/156,487A  
; CURRENT FILING DATE: 2002-09-10  
; PRIOR APPLICATION NUMBER: 60/293,852  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: Patentin ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 500  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-156-487A-6

Query Match 82.1%; Score 2209; DB 14; Length 500;  
Best Local Similarity 81.6%; Pred. No. 9.6e-203;  
Matches 409; Conservative 46; Mismatches 44; Indels 2; Gaps 2;  
Qy 1 MRGELWLL-VLVLRGAARALSPQAGHDEGPGSGWAAGTGVRCWNRRAESPCHVSEPD 59  
Db 1 MRAQLWLLQLLLRGAARALSPATPAGHNEQDSAWTAKTRQGSRRPRESPAQVLKPG 60  
Qy 60 RTQLSQDLGGGTGLAMDTLPDNRTRVVDNHNHYYVSRVYGPSEPHSRRLWVDVAEANSQV 119  
Db 61 KTQLSQDLGGGSLAIDTLPDNRTRVVDNHNHYYVSRVYGPGEKQSQDLWVDLAVANRSHV 120  
Qy 120 KIHTILSNTHROASRVVLSFDFFPGYHPLRQITATGGFIFMGDVIHRMLTATQYVAPLM 179  
Db 121 KIHRILSSSHRQASRVVLSFDFFPGYHPLRQITATGGFIFMGDMLHRMLTATQYVAPLM 180  
Qy 180 ANFNPGYSDNSTVYVFQWQDHVYLQGWEDKGSFTFOAALHHDGRIVPAYKEIP 239  
Db 181 ANFNPGYSDNSTVAYFDNGTVFVQWQDHVYLQDREDRGSFTFOAALHHDGRIVFGYKEIP 240  
Qy 240 MSVPEISSOHVPKVTGLSDAFMILNPSDPVPESSRRSIFEYHRIELDPKVTSMASAVEFT 299





Qy 480 TYAEVPSGHEKEGFMEAEQC 500  
Db 480 TYTEVPSGHEKEGFMEAEQC 500

## RESULT 14

US-09-912-935-36  
; Sequence 36, Application US/09912935  
; Publication No. US20030022825A1  
; GENERAL INFORMATION:  
; APPLICANT: Nishikawa, Mitsuo et al.  
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE  
; FILE REFERENCE: 32066/37483  
; CURRENT APPLICATION NUMBER: US/09/912.935  
; PRIOR FILING DATE: 2001-07-24  
; PRIOR FILING DATE: 2000-12-23  
; NUMBER OF SEQ ID NOS: 53  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 36  
; LENGTH: 431  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-912-935-36

Query Match 81.2%; Score 2185; DB 10; Length 431;  
Best Local Similarity 95.2%; Pred. No. 1.5e-200;  
Matches 416; Conservative 0; Mismatches 7; Indels 14; Gaps 3;

Qy	72	LAMDTLPDNRTRVVEDNHSYVSRLYGSPSPHRELWVDVAEANSQVKIHTILSNTHRQ	131
Db	1	LAMDTLPDNRTRVVEDNHSYVSRLYGSPSPHRELWVDVAEANSQVKIHTILSNTHRQ	60
Qy	132	ASRVVLSDFDPFGHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNST	191
Db	61	ASRVVLSDFDPFGHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNST	120
Qy	192	VVYFDNGTVFVQWDHVYVQWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHP	251
Db	121	VVYFDNGTVFVQWDHVYVQWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHP	180
Qy	252	VKTGLSDAFMLNPSDPVPSRRRSIFEYHRIELDPKVTSMASAVEFTPLTCLQHRSCD	311
Db	181	VKTGLSDAFMLNPSDPVPSRRRSIFEYHRIELDPKVTSMASAVEFTPLTCLQHRSCD	240
Qy	312	ACMSDDLTFNCWCHVLQRCSSGFDTRYQEW-MDYGCAQAEGRMCEDFQD-----ED	363
Db	241	ACMSDDLTFNCWCHVLQRCSSGFDTRYQEWDMGTMGCAQAEAG-----QDVRGLPGMRT	294
Qy	364	HDSASPDTSFSPYDGLTTTSSSLFIDSLTTEDDTKLNPNYAGDGLQNNLSPKTKGTPVH	423
Db	295	TTSASPDTSFSPYDGLTTTSSSLFIDSLTTEDDTKLNPNYAGDGLQNNLSPKTKGTPVH	354
Qy	424	LGTIVGIVLAVLLVAAILLAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPDHSTYAE	483
Db	355	LGTIVGIVLAVLLVAAILLAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPDHSTYAE	414
Qy	484	VEPSGHEKEGFMEAEQC 500	
Db	415	VEPSGHEKEGFMEAEQC 431	

## RESULT 15

US-10-168-365-36  
; Sequence 36, Application US/10168365  
; Publication No. US20030211987A1  
; GENERAL INFORMATION:  
; APPLICANT: Labat, Ivan  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Liu, Chenghua  
; APPLICANT: Childs, John

; APPLICANT: Chao, Cheng-Chi  
; APPLICANT: Drmanac, Radoje T  
; APPLICANT: Mize, Nancy  
; APPLICANT: Lee, Juhli  
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE  
; FILE REFERENCE: 30266/37630  
; CURRENT APPLICATION NUMBER: US/10/168.365  
; CURRENT FILING DATE: 2000-12-22  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 36  
; LENGTH: 431  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-168-365-36

Query Match 81.2%; Score 2185; DB 14; Length 431;  
Best Local Similarity 95.2%; Pred. No. 1.5e-200;  
Matches 416; Conservative 0; Mismatches 7; Indels 14; Gaps 3;

Qy	72	LAMDTLPDNRTRVVEDNHSYVSRLYGSPSPHRELWVDVAEANSQVKIHTILSNTHRQ	131
Db	1	LAMDTLPDNRTRVVEDNHSYVSRLYGSPSPHRELWVDVAEANSQVKIHTILSNTHRQ	60
Qy	132	ASRVVLSDFDPFGHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNST	191
Db	61	ASRVVLSDFDPFGHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNST	120
Qy	192	VVYFDNGTVFVQWDHVYVQWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHP	251
Db	121	VVYFDNGTVFVQWDHVYVQWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHP	180
Qy	252	VKTGLSDAFMLNPSDPVPSRRRSIFEYHRIELDPKVTSMASAVEFTPLTCLQHRSCD	311
Db	181	VKTGLSDAFMLNPSDPVPSRRRSIFEYHRIELDPKVTSMASAVEFTPLTCLQHRSCD	240
Qy	312	ACMSDDLTFNCWCHVLQRCSSGFDTRYQEW-MDYGCAQAEGRMCEDFQD-----ED	363
Db	241	ACMSDDLTFNCWCHVLQRCSSGFDTRYQEWDMGTMGCAQAEAG-----QDVRGLPGMRT	294
Qy	364	HDSASPDTSFSPYDGLTTTSSSLFIDSLTTEDDTKLNPNYAGDGLQNNLSPKTKGTPVH	423
Db	295	TTSASPDTSFSPYDGLTTTSSSLFIDSLTTEDDTKLNPNYAGDGLQNNLSPKTKGTPVH	354
Qy	424	LGTIVGIVLAVLLVAAILLAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPDHSTYAE	483
Db	355	LGTIVGIVLAVLLVAAILLAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPDHSTYAE	414
Qy	484	VEPSGHEKEGFMEAEQC 500	
Db	415	VEPSGHEKEGFMEAEQC 431	

Search completed: January 28, 2005, 22:19:22  
Job time : 138.657 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 28, 2005, 21:52:02 ; Search time 158.818 Seconds  
(without alignments)  
1129.372 Million cell updates/sec

Title: US-09-918-715-230

Perfect score: 2691  
Sequence: 1 MRGELWLLVLVLRARALSL.....YAEVPSGKKGPMFEAQC 500

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 200273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2691	100.0	500	5	ABB90749 Human Tum
2	2691	100.0	500	6	ABU54456 Human tum
3	2691	100.0	500	7	ADI21063 Novel hum
4	2691	100.0	500	8	ADH13230 Human mal
5	2691	100.0	527	7	ADI21554 Novel hum
6	2691	100.0	527	7	ADI21553 Novel hum
7	2691	100.0	1002	5	ABB90723 Human Tum
8	2691	100.0	1002	6	ABU54430 Human tum
9	2607	96.9	488	7	ADI21064 Novel hum
10	2209	82.1	500	5	ABB90783 Mouse Tum
11	2209	82.1	500	5	ABB90729 Mouse Tum
12	2209	82.1	500	6	ABU54436 Mouse tum
13	2209	82.1	500	6	ABU54490 Mouse tum
14	2185	81.2	431	4	RAAB85400 Tumour en
15	2185	81.2	431	6	ABO01434 Human tum
16	2007	74.6	400	3	RAAB43131 Human ORF
17	1295	48.1	499	4	ABAB85396 Stem cell
18	1295	48.1	499	6	ABO01430 Human ste
19	1295	48.1	529	4	ABAB85394 Stem cell
20	1295	48.1	529	5	ABB90734 Human Tum
21	1295	48.1	529	5	ABB90726 Human Tum
22	1295	48.1	529	5	ABP53349 Human tra
23	1295	48.1	529	5	ABG63157 Human ste
24	1295	48.1	529	5	ABG69161 Human pro
25	1295	48.1	529	6	ABU54441 Human tum

26	1295	48.1	529	6	ABU54433	Abu54433 Human tum
27	1295	48.1	529	6	ABO01436	AbO01436 Human ste
28	1295	48.1	529	6	ABO01428	AbO01428 Human ste
29	1295	48.1	529	6	AAE35354	Aae35354 Human TEM
30	1295	48.1	529	8	ADN05749	Adn05749 Antipsoi
31	1294	48.1	529	4	AAAB31211	Ab31211 Amino aci
32	1294	48.1	529	4	AAU29259	Aau29259 Human PRO
33	1294	48.1	529	4	AAAM39068	Aam39068 Human PRO
34	1294	48.1	529	6	ABU58635	Abu58635 Human PRO
35	1294	48.1	529	6	ABU88183	Abu88183 Novel hum
36	1294	48.1	529	6	ABU84498	Abu84498 Human sec
37	1294	48.1	529	6	ABR66372	AbR66372 Human sec
38	1294	48.1	529	6	ABR65762	AbR65762 Human sec
39	1294	48.1	529	6	ABU99702	Abu99702 Human sec
40	1294	48.1	529	6	ABU82941	Abu82941 Human PRO
41	1294	48.1	529	6	ABU90062	Abu90062 Novel hum
42	1294	48.1	529	6	ABR68311	AbR68311 Human hum
43	1294	48.1	529	6	ABU96364	Abu96364 Novel hum
44	1294	48.1	529	6	ABU92795	Abu92795 Human sec
45	1294	48.1	529	6	ABO08872	AbO08872 Human sec

ALIGNMENTS

RESULT 1  
ABB90749  
ID ABB90749 standard; protein; 500 AA.  
XX  
AC ABB90749;  
XX  
DT 30-MAY-2002 (first entry)  
XX  
DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 230.  
XX  
KW Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic;  
KW normal endothelial marker; pan-endothelial marker; immunostimulant;  
KW antiangiogenic; tumour; neoangiogenesis; vascularised tumour;  
KW polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;  
KW psoriasis.  
XX  
OS Homo sapiens.  
XX  
FN WO200210217-A2.  
XX  
PD 07-FEB-2002.  
XX  
PF 01-AUG-2001; 2001WO-US024031.  
XX  
PR 02-AUG-2000; 2000US-0222599P.  
PR 11-AUG-2000; 2000US-0224360P.  
PR 11-APR-2001; 2001US-0282850P.  
XX  
PA (UYJO ) UNIV JOHNS HOPKINS.  
XX  
PI St Croix B, Kinzler KW, Vogelstein B;  
XX  
DR WPI: 2002-291856/33.  
XX  
DR N-PSDB; ABL92103.  
XX  
PT An isolated molecule comprising an antibody variable region which  
PT specifically binds to an extracellular domain of a tumor endothelial  
PT marker (TEM) protein, useful for inhibiting tumor growth.  
XX  
XX  
PS Claim 1; Page 206-207; 31pp; English.  
XX  
CC The invention relates to an isolated molecule comprising an antibody  
CC variable region which specifically binds to an extracellular domain of a  
CC tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740,  
CC ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM  
CC proteins have cytostatic, immunostimulant and antiangiogenic activity.  
CC They are useful for inhibiting tumour growth, neoangiogenesis in subjects  
CC bearing a vascularised tumour, polycystic kidney disease, diabetic

CC retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM  
 CC genes and the encoded proteins (ABL92075-ABL92141 and ABB90721-ABB90789)  
 CC are disclosed, as are marker oligonucleotide sequences: tumour  
 CC endothelial markers (TEM) ABL9196-ABL92041 and ABL92143-ABL92191; normal  
 CC endothelial markers (NEM) ABL92042-ABL92074; and pan-endothelial markers  
 CC (PEM) ABL91903-ABL91995  
 XX  
 XX Sequence 500 AA;

Query Match 100.0%; Score 2691; DB 5; Length 500;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-249;  
 Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 MRGELWLLVLRARALSPQAGHDEGPGSGWAAGTVRGWNRARSPGHVSPDR 60  
 Db 1 MRGELWLLVLRARALSPQAGHDEGPGSGWAAGTVRGWNRARSPGHVSPDR 60  
 Qy 61 TQLSQDLGGGTLMADTLPDNRTRVEDNHSYVVSRLYGPSEPHSRELWVDVAEANRSQVK 120  
 Db 61 TQLSQDLGGGTLMADTLPDNRTRVEDNHSYVVSRLYGPSEPHSRELWVDVAEANRSQVK 120  
 Qy 121 IHTILSNTHRQASRVLSFDFPFYGHPLRQITTIATGGFIFMGDVIHRMLTATQYVAPLMA 180  
 Db 121 IHTILSNTHRQASRVLSFDFPFYGHPLRQITTIATGGFIFMGDVIHRMLTATQYVAPLMA 180  
 Qy 181 NFNPYSDNSTVYVFDNGTVVQWMDHYVLOGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240  
 Db 181 NFNPYSDNSTVYVFDNGTVVQWMDHYVLOGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240  
 Qy 241 SVPEISSQHPVKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKVTSMASVEFTP 300  
 Db 241 SVPEISSQHPVKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKVTSMASVEFTP 300  
 Qy 301 LPTCLQHRSCDACMSSDLTFNCSCWCHVLRQSSGFDYRQEWMDYGCQAEGRMCSDFQ 360  
 Db 301 LPTCLQHRSCDACMSSDLTFNCSCWCHVLRQSSGFDYRQEWMDYGCQAEGRMCSDFQ 360  
 Qy 361 DEHDHSDPSTSFSPYDGLTTTSSSLFIDSLTTEDDTKLNYPAGGGLQNNLSPKTKGT 420  
 Db 361 DEHDHSDPSTSFSPYDGLTTTSSSLFIDSLTTEDDTKLNYPAGGGLQNNLSPKTKGT 420  
 Qy 421 PVHLGTIVGIVLAVLLVAAILLAGIYINGHPTSNAAALFFIERRPHWPAMKFRSHPDHST 480  
 Db 421 PVHLGTIVGIVLAVLLVAAILLAGIYINGHPTSNAAALFFIERRPHWPAMKFRSHPDHST 480  
 Qy 481 YAEVEPSGHEKEGFMFAEQC 500  
 Db 481 YAEVEPSGHEKEGFMFAEQC 500

RESULT 2  
 ABUS4456  
 ID ABUS4456 standard; protein; 500 AA.

XX AC ABUS4456;

XX AC ABUS4456;

DT 12-MAR-2003 (first entry)

XX AC ABUS4456;

XX AC ABUS4456;

DE DE Human tumour endothelial marker TEM 17.

XX KW Human; endothelial cell; EC; tumour endothelial cell; TEM; NEM;

XX KW Tumour endothelial marker; normal endothelial marker; PEM;

XX KW pan-endothelial marker; polycystic kidney disease; psoriasis;

XX KW diabetic retinopathy; rheumatoid arthritis; tumour angiogenesis;

XX KW neovascularization; immune response; cytostatic; antidiabetic;

XX KW ophthalmological; antirheumatic; antiarthritic; antipsoriatic.

OS Homo sapiens.

XX KW Homo sapiens.

XX KW WO200203874-A2.

XX KW 24-OCT-2002.

XX KW

PF 10-APR-2002; 2002WO-US008253.  
 XX  
 PR 11-APR-2001; 2001US-0282850P.  
 PR 06-FEB-2002; 2002US-0354262P.  
 XX  
 PA (UJYO ) UNIV JOHNS HOPKINS.  
 XX  
 XX Carson-Walter E, St Croix B, Kinzler KW, Vogelstein B;  
 XX  
 XX WPI; 2003-093016/08.  
 DR N-PSDB; ABX72028.  
 XX  
 XX New purified human transmembrane protein, designated as tumor endothelial  
 PT marker (TEM) 3, useful for detecting, diagnosing or treating tumors,  
 PT polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis or  
 PT psoriasis.  
 XX  
 PS Disclosure; Page 221-222; 374pp; English.

XX The present invention relates to a novel method for the isolation of  
 CC endothelial cells (ECs), and the identification of genes expressed in  
 CC normal and tumour ECs. Tumour endothelial marker (TEM), normal  
 CC endothelial marker (NEM), and pan-endothelial marker (PEM) genes are  
 CC identified in human ECs. The human EC marker proteins and the  
 CC polynucleotide sequences encoding them are useful for detecting,  
 CC diagnosing or treating tumours as well as polycystic kidney disease,  
 CC diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are also  
 CC useful for inhibiting neovascularization or tumour angiogenesis, for  
 CC inducing an immune response to tumour endothelial cells in a patient, or  
 CC for identifying candidate drugs for treating tumours. The present  
 CC sequence represents a human TEM or NEM protein of the invention  
 XX  
 XX Sequence 500 AA;

Query Match 100.0%; Score 2691; DB 6; Length 500;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-249;  
 Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 MRGELWLLVLRARALSPQAGHDEGPGSGWAAGTVRGWNRARSPGHVSPDR 60  
 Db 1 MRGELWLLVLRARALSPQAGHDEGPGSGWAAGTVRGWNRARSPGHVSPDR 60  
 Qy 61 TQLSQDLGGGTLMADTLPDNRTRVEDNHSYVVSRLYGPSEPHSRELWVDVAEANRSQVK 120  
 Db 61 TQLSQDLGGGTLMADTLPDNRTRVEDNHSYVVSRLYGPSEPHSRELWVDVAEANRSQVK 120  
 Qy 121 IHTILSNTHRQASRVLSFDFPFYGHPLRQITTIATGGFIFMGDVIHRMLTATQYVAPLMA 180  
 Db 121 IHTILSNTHRQASRVLSFDFPFYGHPLRQITTIATGGFIFMGDVIHRMLTATQYVAPLMA 180  
 Qy 181 NFNPYSDNSTVYVFDNGTVVQWMDHYVLOGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240  
 Db 181 NFNPYSDNSTVYVFDNGTVVQWMDHYVLOGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240  
 Qy 241 SVPEISSQHPVKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKVTSMASVEFTP 300  
 Db 241 SVPEISSQHPVKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKVTSMASVEFTP 300  
 Qy 301 LPTCLQHRSCDACMSSDLTFNCSCWCHVLRQSSGFDYRQEWMDYGCQAEGRMCSDFQ 360  
 Db 301 LPTCLQHRSCDACMSSDLTFNCSCWCHVLRQSSGFDYRQEWMDYGCQAEGRMCSDFQ 360  
 Qy 361 DEHDHSDPSTSFSPYDGLTTTSSSLFIDSLTTEDDTKLNYPAGGGLQNNLSPKTKGT 420  
 Db 361 DEHDHSDPSTSFSPYDGLTTTSSSLFIDSLTTEDDTKLNYPAGGGLQNNLSPKTKGT 420  
 Qy 421 PVHLGTIVGIVLAVLLVAAILLAGIYINGHPTSNAAALFFIERRPHWPAMKFRSHPDHST 480  
 Db 421 PVHLGTIVGIVLAVLLVAAILLAGIYINGHPTSNAAALFFIERRPHWPAMKFRSHPDHST 480  
 Qy 481 YAEVEPSGHEKEGFMFAEQC 500  
 Db 481 YAEVEPSGHEKEGFMFAEQC 500

Query Match 100.0%; Score 2691; DB 6; Length 500;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-249;  
 Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 MRGELWLLVLRARALSPQAGHDEGPGSGWAAGTVRGWNRARSPGHVSPDR 60  
 Db 1 MRGELWLLVLRARALSPQAGHDEGPGSGWAAGTVRGWNRARSPGHVSPDR 60  
 Qy 61 TQLSQDLGGGTLMADTLPDNRTRVEDNHSYVVSRLYGPSEPHSRELWVDVAEANRSQVK 120  
 Db 61 TQLSQDLGGGTLMADTLPDNRTRVEDNHSYVVSRLYGPSEPHSRELWVDVAEANRSQVK 120  
 Qy 121 IHTILSNTHRQASRVLSFDFPFYGHPLRQITTIATGGFIFMGDVIHRMLTATQYVAPLMA 180  
 Db 121 IHTILSNTHRQASRVLSFDFPFYGHPLRQITTIATGGFIFMGDVIHRMLTATQYVAPLMA 180  
 Qy 181 NFNPYSDNSTVYVFDNGTVVQWMDHYVLOGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240  
 Db 181 NFNPYSDNSTVYVFDNGTVVQWMDHYVLOGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240  
 Qy 241 SVPEISSQHPVKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKVTSMASVEFTP 300  
 Db 241 SVPEISSQHPVKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKVTSMASVEFTP 300  
 Qy 301 LPTCLQHRSCDACMSSDLTFNCSCWCHVLRQSSGFDYRQEWMDYGCQAEGRMCSDFQ 360  
 Db 301 LPTCLQHRSCDACMSSDLTFNCSCWCHVLRQSSGFDYRQEWMDYGCQAEGRMCSDFQ 360  
 Qy 361 DEHDHSDPSTSFSPYDGLTTTSSSLFIDSLTTEDDTKLNYPAGGGLQNNLSPKTKGT 420  
 Db 361 DEHDHSDPSTSFSPYDGLTTTSSSLFIDSLTTEDDTKLNYPAGGGLQNNLSPKTKGT 420  
 Qy 421 PVHLGTIVGIVLAVLLVAAILLAGIYINGHPTSNAAALFFIERRPHWPAMKFRSHPDHST 480  
 Db 421 PVHLGTIVGIVLAVLLVAAILLAGIYINGHPTSNAAALFFIERRPHWPAMKFRSHPDHST 480  
 Qy 481 YAEVEPSGHEKEGFMFAEQC 500  
 Db 481 YAEVEPSGHEKEGFMFAEQC 500

RESULT 3  
ADI21063  
ID ADI21063 standard; protein; 500 AA.  
XX  
XX  
AC ADI21063;  
XX  
DT 15-APR-2004 (first entry)  
XX  
XX  
DE Novel human protein #38.  
XX  
XX forensic; nutritional source; damaged tissue; diseased tissue;  
KW myeloid cell disorder; lymphoid cell disorder;  
KW bone cartilage tissue growth; tendon tissue growth;  
KW ligament tissue growth; nerve tissue growth; regeneration; wound healing;  
KW tissue repair; tissue replacement; burn; incision; ulcer; cancer; human.  
XX  
OS Homo sapiens.  
XX  
XX WO2003025148-A2.  
XX  
XX  
PD 27-MAR-2003.  
XX  
XX 19-SEP-2002; 2002WO-US029964.  
XX  
XX 19-SEP-2001; 2001US-0323739P.  
XX  
XX 13-SEP-2002; 2002US-00323739.  
XX  
XX (HYSE-) HYSEQ INC.  
XX  
XX Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;  
PI Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang D;  
PI Haley-Vicente D;  
XX  
XX WPI; 2003-354603/33.  
DR N-PSDB; ADI21779.  
XX  
XX New polynucleotides and secreted proteins, useful for treating myeloid or  
PT lymphoid cell disorders, in bone cartilage, tendon, ligament and nerve  
PT tissue growth or regeneration, in wound healing, and in tissue repair and  
PT replacement.  
XX  
XX Claim 20; SEQ ID NO 314; 156pp; English.  
XX  
XX The invention relates to an isolated polynucleotide encoding a  
CC polypeptide with biological activity. The polynucleotides and  
CC polypeptides are useful in diagnostics, forensics, gene mapping, and  
CC identification of mutations responsible for genetic disorders and other  
CC traits, to assess biodiversity, as nutritional sources or supplements.  
CC The polynucleotides may also be used as molecular weight markers,  
CC chromosome markers or map related gene positions, or as an antigen to  
CC raise anti-DNA antibodies or elicit immune response. The polypeptides are  
CC useful for raising antibodies, as markers for tissues in which the  
CC corresponding polypeptide is expressed, for re-engineering damaged or  
CC diseased tissues, for treating myeloid or lymphoid cell disorders, in  
CC bone cartilage, tendon, ligament and/or nerve tissue growth or  
CC regeneration, in wound healing, in tissue repair and replacement, in  
CC healing of burns, incisions and ulcers, and in treating cancer. The  
CC present sequence represents the amino acid sequence of a novel human  
XX protein.  
XX  
SQ Sequence 500 AA;  
Query Match 100.0%; Score 2691; DB 7; Length 500;  
Best Local Similarity 100.0%; Pred. No. 3.1e-249;  
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MRGELWLLVLVLRRAALSPQAGAGHDEGPGSCWAAGTGVGNRRARSPGHVSEPD 60  
DB 1 MRGELWLLVLVLRRAALSPQAGAGHDEGPGSCWAAGTGVGNRRARSPGHVSEPD 60  
QY 61 TQLSQDLGGGTFLAMDITLDPNRTVVEDNHSYYSRLYGPSEPHSRELWVDVAENRSQVK 120

Db 61 TQLSQDLGGGTFLAMDITLDPNRTVVEDNHSYYSRLYGPSEPHSRELWVDVAENRSQVK 120  
QY 121 IHTILSNTHRQASRVLSFDFFPYGHPLRQITATGGFIEMGDVIHRMLTATQVAPLMA 180  
Db 121 IHTILSNTHRQASRVLSFDFFPYGHPLRQITATGGFIEMGDVIHRMLTATQVAPLMA 180  
QY 181 NFNPGYSDNSTVYFDNGTVFVQWMDHVLQGWEDKGSFTFQAALHHDGRIVFAYPEIPM 240  
Db 181 NFNPGYSDNSTVYFDNGTVFVQWMDHVLQGWEDKGSFTFQAALHHDGRIVFAYPEIPM 240  
QY 241 SVPEISSQHPVKTGLSDAFMILNPSDPVPSRERSIFEYHRIELDSPKVTSMASVETP 300  
Db 241 SVPEISSQHPVKTGLSDAFMILNPSDPVPSRERSIFEYHRIELDSPKVTSMASVETP 300  
QY 301 LPTCLQHRSCDACMSSDLTFNCSCWCHVLQRCSSGFDRYQEWMDYGCQAQEAEGRMCEDFQ 360  
Db 301 LPTCLQHRSCDACMSSDLTFNCSCWCHVLQRCSSGFDRYQEWMDYGCQAQEAEGRMCEDFQ 360  
QY 361 DEHDSASPTSPSPYDGLTTTSSSLFIDSLTTEDDTKLNYPYAGDGLQNNLSPKTKGT 420  
Db 361 DEHDSASPTSPSPYDGLTTTSSSLFIDSLTTEDDTKLNYPYAGDGLQNNLSPKTKGT 420  
QY 421 PVHLGTTIVGIVLAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPDHST 480  
Db 421 PVHLGTTIVGIVLAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPDHST 480  
QY 481 YAEVEPSGHEKEGFMEAEQC 500  
Db 481 YAEVEPSGHEKEGFMEAEQC 500  
RESULT 4  
ADH13230  
ID ADH13230 standard; protein; 500 AA.  
XX  
AC ADH13230;  
XX  
DT 11-MAR-2004 (first entry)  
XX  
DE Human malignant neoplasia-related protein SeqID79.  
XX  
KW malignant neoplasia; cytostatic; breast cancer; ovarian cancer;  
KW gastric cancer; colon cancer; oesophageal cancer; mesenchymal cancer;  
KW bladder cancer; non-small cell lung cancer; human.  
OS Homo sapiens.  
XX  
XX EPI365034-A2.  
XX  
PD 26-NOV-2003.  
XX  
PF 09-MAY-2003; 2003EP-00010447.  
XX  
PR 21-MAY-2002; 2002EP-00010291.  
PR 13-FEB-2003; 2003EP-00003112.  
XX  
PA (FARB ) BAYER AG.  
XX  
XX Wirtz R, Munnes M, Kallabis H;  
XX  
DR WPI; 2004-073279/08.  
DR N-PSDB; ADH13207.  
XX  
XX Predicting, diagnosing or prognosing malignant neoplasia by detecting at  
FT least two markers, where the markers are genes from one or more  
FT chromosomal regions altered in malignant neoplasia.  
XX  
XX Claim 11; SEQ ID NO 79; 267pp; English.  
XX  
XX This invention relates to a novel method for the prediction, diagnosis,  
CC or prognosis of malignant neoplasia by the detection of at least two  
CC markers. The invention may also be useful for the development of

CC cytostatic compounds through the regulation of the expression of a gene  
 CC or activity of a protein associated with malignant neoplasia. The method  
 CC is useful for prediction, diagnosis or prognosis of malignant neoplasia  
 CC such as breast cancer, ovarian cancer, gastric cancer, colon cancer,  
 CC esophageal cancer, mesenchymal cancer, bladder cancer or non-small cell  
 CC lung cancer. The polynucleotides and polypeptides defined in the  
 CC specification, antisense polynucleotides targeting the polynucleotides,  
 CC antibodies targeting either one of the polynucleotides or polypeptides,  
 CC and compounds identified by the screening methods are useful for  
 CC preventing or treating malignant neoplasia. The disease treated is  
 CC preferably breast cancer. The present sequence is that of a human  
 CC malignant neoplasia-related protein which may be used in the method of  
 CC the invention.

XX  
 SQ Sequence 500 AA;

Query Match 100.0%; Score 2691; DB 8; Length 500;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-249;  
 Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRGELWLLVLVLEAARALSPQAGHDEGPGSGWAAGTGVGNRRRARESPGHVSEPD 60  
 Db 1 MRGELWLLVLVLEAARALSPQAGHDEGPGSGWAAGTGVGNRRRARESPGHVSEPD 60  
 Qy 61 TQLSODLGGGTAMDITLDPNTRVVEDNHSYVSRLYGSPHRELWVDVAEANRSQVK 120  
 Db 61 TQLSODLGGGTAMDITLDPNTRVVEDNHSYVSRLYGSPHRELWVDVAEANRSQVK 120  
 Qy 121 IHTILSNTHRQASRVLSDFPFYGHPLRQITATGGFIFMGDVHRLMTATQYVAPLMA 180  
 Db 121 IHTILSNTHRQASRVLSDFPFYGHPLRQITATGGFIFMGDVHRLMTATQYVAPLMA 180  
 Qy 181 NFNGYSDNSTVYVFDNGTVFVQWDHYVLOGWEDKGSFTQAAALHHDGRIVFAYKEIPM 240  
 Db 181 NFNGYSDNSTVYVFDNGTVFVQWDHYVLOGWEDKGSFTQAAALHHDGRIVFAYKEIPM 240  
 Qy 241 SVPEISSQHPVKTKGLSDAFMLNPSDPVPSRRRSIFEYHRIELDPKVTSMASVEFTP 300  
 Db 241 SVPEISSQHPVKTKGLSDAFMLNPSDPVPSRRRSIFEYHRIELDPKVTSMASVEFTP 300  
 Qy 301 LPTCLQHRSCDACMSSDLTFNCSCWCHVLQRCSSGFDRYQEWMDYGCQAEGRMCEDFQ 360  
 Db 301 LPTCLQHRSCDACMSSDLTFNCSCWCHVLQRCSSGFDRYQEWMDYGCQAEGRMCEDFQ 360  
 Qy 361 DEDHDSASPDTSFSPYDGDLTFTSSSLFIDSLTTEDDTKLPYAGGDLQNNLSPKTKGT 420  
 Db 361 DEDHDSASPDTSFSPYDGDLTFTSSSLFIDSLTTEDDTKLPYAGGDLQNNLSPKTKGT 420  
 Qy 421 PVHLGTIGIVLAVLLVAAIILAGIYINGHPTSNAALEFFIERRPHWPAKFRSHPDHST 480  
 Db 421 PVHLGTIGIVLAVLLVAAIILAGIYINGHPTSNAALEFFIERRPHWPAKFRSHPDHST 480  
 Qy 481 YAEVEPSGHEKEGFMEAEQC 500  
 Db 481 YAEVEPSGHEKEGFMEAEQC 500

RESULT 5

AD121554  
 ID AD121554 standard; protein; 527 AA.

XX  
 AC AD121554;

XX 15-APR-2004 (first entry)

DE Novel human polypeptide #33.

XX forensic; nutritional source; damaged tissue; diseased tissue;  
 KW myeloid cell disorder; lymphoid cell disorder;  
 KW bone cartilage tissue growth; tendon tissue growth;  
 KW ligament tissue growth; nerve tissue growth; regeneration; wound healing;  
 KW tissue repair; tissue replacement; burn; incision; ulcer; cancer; human.

OS Homo sapiens.

XX WO2003025148-A2.

XX 27-MAR-2003.

XX 19-SEP-2002; 2002WO-US029964.

XX 19-SEP-2001; 2001US-0323739P.

XX 13-SEP-2002; 2002US-00323739.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Aeundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;  
 PI Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang D;  
 PI Haley-Vicente D;

XX WPI; 2003-354603/33.

XX N-PSDB; ADI21334.

XX New polynucleotides and secreted proteins, useful for treating myeloid or  
 PT lymphoid cell disorders, in bone cartilage, tendon, ligament and nerve  
 PT tissue growth or regeneration, in wound healing, and in tissue repair and  
 PT replacement.

XX Example 3; SEQ ID NO 805; 156pp; English.

XX The invention relates to an isolated polynucleotide encoding a  
 CC polypeptide with biological activity. The polynucleotides and  
 CC polypeptides are useful in diagnostics, forensics, gene mapping,  
 CC identification of mutations responsible for genetic disorders and other  
 CC traits, to assess biodiversity, as nutritional sources or supplements.  
 CC The polynucleotides may also be used as molecular weight markers,  
 CC chromosome markers or map related gene positions, or as an antigen to  
 CC raise anti-DNA antibodies or elicit immune response. The polypeptides are  
 CC useful for raising antibodies, as markers for tissues in which the  
 CC corresponding polypeptide is expressed, for re-engineering damaged or  
 CC diseased tissues, for treating myeloid or lymphoid cell disorders, in  
 CC bone cartilage, tendon, ligament and/or nerve tissue growth or  
 CC regeneration, in wound healing, in tissue repair and replacement, in  
 CC healing of burns, incisions and ulcers, and in treating cancer. The  
 CC present sequence represents the amino acid sequence of a novel human  
 CC polypeptide.

XX Sequence 527 AA;

Query Match 100.0%; Score 2691; DB 7; Length 527;

Best Local Similarity 100.0%; Pred. No. 3.3e-249;

Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRGELWLLVLVLEAARALSPQAGHDEGPGSGWAAGTGVGNRRRARESPGHVSEPD 60  
 Db 28 MRGELWLLVLVLEAARALSPQAGHDEGPGSGWAAGTGVGNRRRARESPGHVSEPD 87  
 Qy 61 TQLSODLGGGTAMDITLDPNTRVVEDNHSYVSRLYGSPHRELWVDVAEANRSQVK 120  
 Db 88 TQLSODLGGGTAMDITLDPNTRVVEDNHSYVSRLYGSPHRELWVDVAEANRSQVK 147  
 Qy 121 IHTILSNTHRQASRVLSDFPFYGHPLRQITATGGFIFMGDVHRLMTATQYVAPLMA 180  
 Db 148 IHTILSNTHRQASRVLSDFPFYGHPLRQITATGGFIFMGDVHRLMTATQYVAPLMA 207  
 Qy 181 NFNGYSDNSTVYVFDNGTVFVQWDHYVLOGWEDKGSFTQAAALHHDGRIVFAYKEIPM 240  
 Db 208 NFNGYSDNSTVYVFDNGTVFVQWDHYVLOGWEDKGSFTQAAALHHDGRIVFAYKEIPM 267  
 Qy 241 SVPEISSQHPVKTKGLSDAFMLNPSDPVPSRRRSIFEYHRIELDPKVTSMASVEFTP 300  
 Db 268 SVPEISSQHPVKTKGLSDAFMLNPSDPVPSRRRSIFEYHRIELDPKVTSMASVEFTP 327  
 Qy 301 LPTCLQHRSCDACMSSDLTFNCSCWCHVLQRCSSGFDRYQEWMDYGCQAEGRMCEDFQ 360  
 Db 328 LPTCLQHRSCDACMSSDLTFNCSCWCHVLQRCSSGFDRYQEWMDYGCQAEGRMCEDFQ 387

Qy 361 DEDHDSASPTSPSPYDGLTSSSLFIDSLTTEDDTKLNYPYAGDGLQNNLSPKTKGT 420  
Db 388 DEDHDSASPTSPSPYDGLTSSSLFIDSLTTEDDTKLNYPYAGDGLQNNLSPKTKGT 447  
Qy 421 PVHLGTTIGIVLAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPDHST 480  
Db 448 PVHLGTTIGIVLAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPDHST 507  
Qy 481 YAEVEPSGHEKEGFMEAEQC 500  
Db 508 YAEVEPSGHEKEGFMEAEQC 527

RESULT 6  
ADI21553  
ID ADI21553 standard; protein; 527 AA.  
XX AC ADI21553;  
XX 15-APR-2004 (first entry)  
XX DE Novel human polypeptide #32.  
XX KW forensic; nutritional source; damaged tissue; diseased tissue;  
KW myeloid cell disorder; lymphoid cell disorder;  
KW bone cartilage tissue growth; tendon tissue growth;  
KW ligament tissue growth; nerve tissue growth; regeneration; wound healing;  
KW tissue repair; tissue replacement; burn; incision; ulcer; cancer; human.  
XX OS Homo sapiens.  
XX PN WO2003025148-A2.  
XX PD 27-MAR-2003.  
XX PF 19-SEP-2002; 2002WO-US029964.  
XX PR 19-SEP-2001; 2001US-0323739P.  
XX PR 13-SEP-2002; 2002US-00323739.  
XX PA (HYSE-) HYSEQ INC.  
XX PI Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;  
PI Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang D;  
PI Haley-Vicente D;  
XX WPI; 2003-354603/33.  
XX DR N-PSDB; ADI21333.  
XX PT New polynucleotides and secreted proteins, useful for treating myeloid or  
PT lymphoid cell disorders, in bone cartilage, tendon, ligament and nerve  
PT tissue growth or regeneration, in wound healing, and in tissue repair and  
PT replacement.  
XX PS Example 3; SEQ ID NO 804; 156pp; English.  
XX CC The invention relates to an isolated polynucleotide encoding a  
CC polypeptide with biological activity. The polynucleotides and  
CC polypeptides are useful in diagnostics, forensics, gene mapping, and  
CC identification of mutations responsible for genetic disorders and other  
CC traits, to assess biodiversity, as nutritional sources or supplements.  
CC The polynucleotides may also be used as molecular weight markers,  
CC chromosome markers or map related gene positions, or as an antigen to  
CC raise anti-DNA antibodies or elicit immune response. The polypeptides are  
CC useful for raising antibodies, as markers for tissues in which the  
CC corresponding polypeptide is expressed, for re-engineering damaged or  
CC diseased tissues, for treating myeloid or lymphoid cell disorders, in  
CC bone cartilage, tendon, ligament and/or nerve tissue growth or  
CC regeneration, in wound healing, in tissue repair and replacement, in  
CC healing of burns, incisions and ulcers, and in treating cancer. The  
CC present sequence represents the amino acid sequence of a novel human  
CC polypeptide.

XX SQ Sequence 527 AA;  
Query Match 100.0%; Score 2691; DB 7; Length 527;  
Best Local Similarity 100.0%; Pred. No. 3 3e-249;  
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MRGELWLLVLVLRRAARALSPQCGAGHDEPGSGAAAKGTVRGNRRARSPGHVSEPR 60  
Db 28 MRGELWLLVLVLRRAARALSPQCGAGHDEPGSGAAAKGTVRGNRRARSPGHVSEPR 87  
Qy 61 TQLSODLGGGTLMADTLPDNRTRVVDNHSYVYSRLYGPSPHSHRELWVDVAENRSQVK 120  
Db 88 TQLSODLGGGTLMADTLPDNRTRVVDNHSYVYSRLYGPSPHSHRELWVDVAENRSQVK 147  
Qy 121 IHTILSNTHROASRVLSFDFFPGHPLRQITATGCFIPMGDVIHRMLTATQVAPLMA 180  
Db 148 IHTILSNTHROASRVLSFDFFPGHPLRQITATGCFIPMGDVIHRMLTATQVAPLMA 207  
Qy 181 NFNPYSDNSTVYVFDNGTVFVQWDHVLQGWEDKGSFTFQAAALHHDGRIVFAYKEIPM 240  
Db 208 NFNPYSDNSTVYVFDNGTVFVQWDHVLQGWEDKGSFTFQAAALHHDGRIVFAYKEIPM 267  
Qy 241 SVPEISSQHPVKTGLSDAFMILNPSDPVPESRRSIFEYHRIELDSPKVTMSAVEFTP 300  
Db 268 SVPEISSQHPVKTGLSDAFMILNPSDPVPESRRSIFEYHRIELDSPKVTMSAVEFTP 327  
Qy 301 LPTCLQHRSCDACMSDLTFNCSCWCHVLRQCSSGFDRYQROEMDYGCAQAEGRMCEDFQ 360  
Db 328 LPTCLQHRSCDACMSDLTFNCSCWCHVLRQCSSGFDRYQROEMDYGCAQAEGRMCEDFQ 387  
Qy 361 DEHDHDSASPTSPSPYDGLTSSSLFIDSLTTEDDTKLNYPYAGDGLQNNLSPKTKGT 420  
Db 388 DEHDHDSASPTSPSPYDGLTSSSLFIDSLTTEDDTKLNYPYAGDGLQNNLSPKTKGT 447  
Qy 421 PVHLGTTIGIVLAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPDHST 480  
Db 448 PVHLGTTIGIVLAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPDHST 507  
Qy 481 YAEVEPSGHEKEGFMEAEQC 500  
Db 508 YAEVEPSGHEKEGFMEAEQC 527

RESULT 7  
ABB90723  
ID ABB90723 standard; protein; 1002 AA.  
XX AC ABB90723;  
XX 30-MAY-2002 (first entry)  
XX DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 179.  
XX KW Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic;  
KW normal endothelial marker; pan-endothelial marker; immunostimulant;  
KW antiangiogenic; tumour; neoangiogenesis; vascularised tumour;  
KW polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;  
KW psoriasis.  
XX OS Homo sapiens.  
XX PN WO200210217-A2.  
XX PD 07-FEB-2002;  
XX PF 01-AUG-2001; 2001WO-US024031.  
XX PR 02-AUG-2000; 2000US-0222599P.  
XX PR 11-AUG-2000; 2000US-0224360P.  
XX PR 11-APR-2001; 2001US-0282850P.  
XX PA (UYJO ) UNIV JOHNS HOPKINS.

```

XX St Croix B, Kinzler KW, Vogelstein B;
XX WPI; 2002-291856/33.
XX
XX An isolated molecule comprising an antibody variable region which
XX specifically binds to an extracellular domain of a tumor endothelial
XX marker (TEM) protein, useful for inhibiting tumor growth.
XX
XX Disclosure; Page 125-128; 331pp; English.
XX
XX The invention relates to an isolated molecule comprising an antibody
XX variable region which specifically binds to an extracellular domain of a
XX tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740,
XX ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM
XX proteins have cytostatic, immunostimulant and antiangiogenic activity.
XX They are useful for inhibiting tumour growth, neoangiogenesis in subjects
XX bearing a vascularised tumour, polycystic kidney disease, diabetic
XX retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM
XX genes and the encoded proteins (ABL92075-ABL92141 and ABB90721-ABB90789)
XX are disclosed, as are marker oligonucleotide sequences: tumour
XX endothelial markers (TEM) ABL91996-ABL92041 and ABL92143-ABL92191; normal
XX endothelial markers (NEM) ABL92042-ABL92074; and pan-endothelial markers
XX (PEM) ABL91903-ABL91995
XX
XX Sequence 1002 AA;
XX
XX Query Match 100.0%; Score 2691; DB 5; Length 1002;
XX Best Local Similarity 100.0%; Pred. No. 9e-249;
XX Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Qy 1 MRGELWLLVLRRAARALSPQCGAGHDEGPGSGWAAGTGVGNRRARSPGHVSPDR 60
Db |||||||
Qy 503 MRGELWLLVLRRAARALSPQCGAGHDEGPGSGWAAGTGVGNRRARSPGHVSPDR 562
Db |||||||
Qy 61 TQSQDLGGGTGLAMDTLPDNRTRVVEDNHSYVSRLYGSPSPHRELWVDVAEANRSQVK 120
Db |||||||
Qy 563 TQSQDLGGGTGLAMDTLPDNRTRVVEDNHSYVSRLYGSPSPHRELWVDVAEANRSQVK 622
Db |||||||
Qy 121 IHTILSNTHRQASRVLSFDPPFYGHPLRQITTIATGGFIFMGDVHRLMTATQYVAPLMA 180
Db |||||||
Qy 623 IHTILSNTHRQASRVLSFDPPFYGHPLRQITTIATGGFIFMGDVHRLMTATQYVAPLMA 682
Db |||||||
Qy 181 NFNPYSDNSTVYFDNGTVFVQWDHVYLOGWEDKGSFTFOALHHDGRIVFAYKEIPM 240
Db |||||||
Qy 683 NFNPYSDNSTVYFDNGTVFVQWDHVYLOGWEDKGSFTFOALHHDGRIVFAYKEIPM 742
Db |||||||
Qy 241 SVPEISSQHPVKTKGLSDFAMILNPSPDVPSRRRSIFEYHRIELDPKTSMSAVEFTP 802
Db |||||||
Qy 301 LPTCLQHRSCDACMSSDLTFNCSCWCHVLQRCSSGFDYRQEMWYGCQAEGRMCDPQ 360
Db |||||||
Qy 803 LPTCLQHRSCDACMSSDLTFNCSCWCHVLQRCSSGFDYRQEMWYGCQAEGRMCDPQ 862
Db |||||||
Qy 361 DEDHDSAPDTSRSPYDGLTTSSLPIDSLTTEDDTKLPYAGGDLQNNLSPKTKGT 420
Db |||||||
Qy 863 DEDHDSAPDTSRSPYDGLTTSSLPIDSLTTEDDTKLPYAGGDLQNNLSPKTKGT 922
Db |||||||
Qy 421 PVHLGTIVGIVLAVLLVAAIILAGIYINGHTPSNAALFFIERRPHWPAMKFRSHPDHST 480
Db |||||||
Qy 923 PVHLGTIVGIVLAVLLVAAIILAGIYINGHTPSNAALFFIERRPHWPAMKFRSHPDHST 982
Db |||||||
Qy 481 YAEVPSGHEKEGFMFAEQC 500
Db |||||||
Qy 983 YAEVPSGHEKEGFMFAEQC 1002
Db |||||||
XX
XX RESULT 8
XX ABUS4430
XX ID ABUS4430 standard; protein; 1002 AA.
XX
XX AC ABUS4430;

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XX 12-MAR-2003 (first entry)
XX Human tumour endothelial marker TEM 8.
XX
XX Human; endothelial cell; EC; tumour endothelial cell; TEM; NEM;
XX Tumour endothelial marker; normal endothelial marker; PEM;
XX pan-endothelial marker; polycystic kidney disease; psoriasis;
XX diabetic retinopathy; rheumatoid arthritis; tumour angiogenesis;
XX neoangiogenesis; immune response; cytotatic; antidiabetic;
XX ophthalmological; antirheumatic; antiarthritic; antipsoriatic.
XX
XX Homo sapiens.
XX
XX WO200283874-A2.
XX
XX 24-OCT-2002.
XX
XX 10-APR-2002; 2002WO-US008253.
XX
XX 11-APR-2001; 2001US-0282850P.
XX 06-FEB-2002; 2002US-0354262P.
XX
XX (UYJO ) UNIV JOHNS HOPKINS.
XX
XX Carson-Walter E, St Croix B, Kinzler KW, Vogelstein B;
XX
XX WPI; 2003-093016/08.
XX N-PSDB; ABX72003.
XX
XX New purified human transmembrane protein, designated as tumor endothelial
XX marker (TEM) 3, useful for detecting, diagnosing or treating tumors,
XX polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis or
XX psoriasis.
XX
XX Disclosure; Page 122-124; 374pp; English.
XX
XX The present invention relates to a novel method for the isolation of
XX endothelial cells (ECs), and the identification of genes expressed in
XX normal and tumour ECs. Tumour endothelial marker (TEM), normal
XX endothelial marker (NEM), and pan-endothelial marker (PEM) genes are
XX identified in human ECs. The human EC marker proteins and the
XX polynucleotide sequences encoding them are useful for detecting,
XX diagnosing or treating tumors as well as polycystic kidney disease,
XX diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are also
XX useful for inhibiting neoangiogenesis or tumour angiogenesis, for
XX inducing an immune response to tumour endothelial cells in a patient, or
XX for identifying candidate drugs for treating tumours. The present
XX sequence represents a human TEM or NEM protein of the invention
XX
XX Sequence 1002 AA;
XX
XX Query Match 100.0%; Score 2691; DB 6; Length 1002;
XX Best Local Similarity 100.0%; Pred. No. 9e-249;
XX Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Qy 1 MRGELWLLVLRRAARALSPQCGAGHDEGPGSGWAAGTGVGNRRARSPGHVSPDR 60
Db |||||||
Qy 503 MRGELWLLVLRRAARALSPQCGAGHDEGPGSGWAAGTGVGNRRARSPGHVSPDR 562
Db |||||||
Qy 61 TQSQDLGGGTGLAMDTLPDNRTRVVEDNHSYVSRLYGSPSPHRELWVDVAEANRSQVK 120
Db |||||||
Qy 563 TQSQDLGGGTGLAMDTLPDNRTRVVEDNHSYVSRLYGSPSPHRELWVDVAEANRSQVK 622
Db |||||||
Qy 121 IHTILSNTHRQASRVLSFDPPFYGHPLRQITTIATGGFIFMGDVHRLMTATQYVAPLMA 180
Db |||||||
Qy 623 IHTILSNTHRQASRVLSFDPPFYGHPLRQITTIATGGFIFMGDVHRLMTATQYVAPLMA 682
Db |||||||
Qy 181 NFNPYSDNSTVYFDNGTVFVQWDHVYLOGWEDKGSFTFOALHHDGRIVFAYKEIPM 240
Db |||||||
Qy 683 NFNPYSDNSTVYFDNGTVFVQWDHVYLOGWEDKGSFTFOALHHDGRIVFAYKEIPM 742
Db |||||||
Qy 241 SVPEISSQHPVKTKGLSDFAMILNPSPDVPSRRRSIFEYHRIELDPKTSMSAVEFTP 300
Db |||||||

```

Db 743 SVPEISSQHPVKTLGSLDAFNLNPSDPVPSRRRSIFEHRIELDPKSVTMSAVEFTP 802  
 Qy 301 LPTCLQHRSCDACMSSDLTFNCWCHVLQRCSSGFDYRQEWMDYGCQAEGRMCEDFQ 360  
 Db 803 LPTCLQHRSCDACMSSDLTFNCWCHVLQRCSSGFDYRQEWMDYGCQAEGRMCEDFQ 862  
 Qy 361 DEDHDSASPDTSFSPYDGLTFTSSSLFIDSLTDEDDTKLNPYAGDGLQNNLSPKTKGT 420  
 Db 863 DEDHDSASPDTSFSPYDGLTFTSSSLFIDSLTDEDDTKLNPYAGDGLQNNLSPKTKGT 922  
 Qy 421 PVHLGTVIGIVLAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPDHST 480  
 Db 923 PVHLGTVIGIVLAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPDHST 982  
 Qy 481 YAEVEPSGHEKEGFMEAEQC 500  
 Db 983 YAEVEPSGHEKEGFMEAEQC 1002

## RESULT 9

ADI21064  
 ID ADI21064 standard; protein; 488 AA.

AC ADI21064;

XX 15-APR-2004 (first entry)

XX Novel human protein #39.

XX forensic; nutritional source; damaged tissue; disease tissue;  
 KW myeloid cell disorder; lymphoid cell disorder;  
 KW bone cartilage tissue growth; tendon tissue growth;  
 KW ligament tissue growth; nerve tissue growth; regeneration; wound healing;  
 KW tissue repair; tissue replacement; burn; incision; ulcer; cancer; human.

OS Homo sapiens.

FN WO2003025148-A2.

XX 27-MAR-2003.

XX 19-SEP-2002; 2002WO-US029964.

XX 19-SEP-2001; 2001US-0323739P.

PR 13-SEP-2002; 2002US-00323739.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;  
 PI Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang D;  
 XX Haley-Vicente D;

DR WPI; 2003-354603/33.

DR N-PSDB; ADI21780.

XX New polynucleotides and secreted proteins, useful for treating myeloid or  
 PT lymphoid cell disorders, in bone cartilage, tendon, ligament and nerve  
 PT tissue growth or regeneration, in wound healing, and in tissue repair and  
 PT replacement.

XX Claim 20; SEQ ID NO 315; 156pp; English.

XX The invention relates to an isolated polynucleotide encoding a  
 CC polypeptide with biological activity. The polynucleotides and  
 CC polypeptides are useful in diagnostics, forensics, gene mapping,  
 CC identification of mutations responsible for genetic disorders and other  
 CC traits, to assess biodiversity, as nutritional sources or supplements.  
 CC The polynucleotides may also be used as molecular weight markers,  
 CC chromosome markers or map related gene positions, or as an antigen to  
 CC raise anti-DNA antibodies or elicit immune response. The polypeptides are  
 CC useful for raising antibodies, as markers for tissues in which the  
 CC corresponding polypeptide is expressed, for re-engineering damaged or

CC diseased tissues, for treating myeloid or lymphoid cell disorders, in  
 CC bone cartilage, tendon, ligament and/or nerve tissue growth or  
 CC regeneration, in wound healing, in tissue repair and replacement, in  
 CC healing of burns, incisions and ulcers, and in treating cancer. The  
 CC present sequence represents the amino acid sequence of a novel human  
 CC protein.

XX SQ Sequence 488 AA;

Query Match 96.9%; Score 2607; DB 7; Length 488;

Best Local Similarity 97.6%; Pred. No. 3.5e-241;

Matches 488; Conservative 0; Mismatches 0; Indels 12; Gaps 1;

Qy 1 MRGELWLLVLRREARALSPQAGHDEGPGSCWAAKGTVRGNRRARESPGHVSEPD 60

Db 1 MRGELWLLVLRREARALSPQAGHDEGPGSCWAAKGTVRGNRRARESPGHVSEPD 60

Qy 61 TQLSQDLGGGTFLAMDITLFDNRTRVVDNHSYVSRLYGSPSPHRELWVDVAENRSQVK 120

Db 61 TQLSQDLGGGTFLAMDITLFDNRTRVVDNHSYVSRLYGSPSPHRELWVDVAENRSQVK 120

Qy 121 IHTILSNTHRQASRVLSFDPPFYGHPLRQITTIATGGFIFMGDVIHRMLTATQYVAPLMA 180

Db 121 IHTILSNTHRQASRVLSFDPPFYGHPLRQITTIATGGFIFMGDVIHRMLTATQYVAPLMA 180

Qy 181 NFPGYSDNSTVYFDNGTVFVQMDHYVLQGWEDKGSFTFQAAALHHDGRIVFAYKEIPM 240

Db 181 NFPGYSDNSTVYFDNGTVFVQMDHYVLQGWEDKGSFTFQAAALHHDGRIVFAYKEIPM 240

Qy 241 SVPEISSQHPVKTLGSLDAFNLNPSDPVPSRRRSIFEHRIELDPKSVTMSAVEFTP 300

Db 241 SVPEISSQHPVKTLGSLDAFNLNPSDPVPSRRRSIFEHRIELDPKSVTMSAVEFTP 300

Qy 301 LPTCLQHRSCDACMSSDLTFNCWCHVLQRCSSGFDYRQEWMDYGCQAEGRMCEDFQ 360

Db 301 LPTCLQHRSCDACMSSDLTFNCWCHVLQRCSSGFDYRQEWMDYGCQAEGRMCEDFQ 360

Qy 361 DEDHDSASPDTSFSPYDGLTFTSSSLFIDSLTDEDDTKLNPYAGDGLQNNLSPKTKGT 420

Db 361 DEDHDSASPDTSFSPYDGLTFTSSSLFIDSLTDEDDTKLNPYAGDGLQNNLSPKTKGT 420

Qy 421 PVHLGTVIGIVLAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPDHST 480

Db 409 PVHLGTVIGIVLAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPDHST 468

Qy 481 YAEVEPSGHEKEGFMEAEQC 500

Db 469 YAEVEPSGHEKEGFMEAEQC 488

RESULT 10  
 ABB90783  
 ID ABB90783 standard; protein; 500 AA.

XX AC ABB90783;

XX 30-MAY-2002 (first entry)

DE Mouse Tumour Endothelial Marker polypeptide SEQ ID NO 297.

XX Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic;  
 KW normal endothelial marker; pan-endothelial marker; immunostimulant;  
 KW antiangiogenic; tumour; neoangiogenesis; vascularised tumour;  
 KW polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;  
 KW psoriasis.

XX Mus musculus.

XX WO200210217-A2.

XX 07-FEB-2002.

XX 01-AUG-2001; 2001WO-US024031.



XX 02-AUG-2000; 2000US-0222599P.  
PR 11-AUG-2000; 2000US-0224360P.  
PR 11-APR-2001; 2001US-0282850P.  
XX (UYJO ) UNIV JOHNS HOPKINS.  
XX St Croix B, Kinzler KW, Vogelstein B;  
XX WPI; 2002-291856/33.  
XX N-PSDB; ABL92136.  
XX An isolated molecule comprising an antibody variable region which  
PT specifically binds to an extracellular domain of a tumor endothelial  
PT marker (TEM) protein, useful for inhibiting tumor growth.  
XX  
XX  
PS Disclosure; Page 301-302; 331pp; English.  
XX  
XX The invention relates to an isolated molecule comprising an antibody  
CC variable region which specifically binds to an extracellular domain of a  
CC tumor endothelial marker (TEM) protein selected from ABB90732, ABB90740,  
CC ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM  
CC proteins have cytostatic, immunostimulant and antiangiogenic activity.  
CC They are useful for inhibiting tumor growth, neoangiogenesis in subjects  
CC bearing a vascularised tumour, polycystic kidney disease, diabetic  
CC retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM  
CC genes and the encoded proteins (ABL92075-ABL92141 and ABB90721-ABB90789)  
CC are disclosed, as are marker oligonucleotide sequences: tumour  
CC endothelial markers (TEM) ABL91996-ABL92041 and ABL92143-ABL92191; normal  
CC endothelial markers (NEM) ABL92042-ABL92074; and pan-endothelial markers  
CC (PEM) ABL91903-ABL91995  
XX  
SQ Sequence 500 AA;  
  
Query Match 82.1%; Score 2209; DB 5; Length 500;  
Best Local Similarity 81.6%; Pred. No. 6.7e-203;  
Matches 409; Conservative 46; Mismatches 44; Indels 2; Gaps 2;  
  
Qy 1 MRGLWLL-L-VLVLEAARALSPQAGHDEGPGSGWAAGTVRCGNRRARSPGHVSEPD 59  
Db 1 MRAQLWLLQLLLKGAARALSPATPAGHNEQDQSAWTAKTTRQGSRRPRSPQAVLKP 60  
  
Qy 60 RTQLSQDLGGGTGLAMDTLPDNRTRVVEDNHNHYSRLYGPSEPHSRLWVDVAENRSQV 119  
Db 61 KTQLSQDLGGGSLAIDLTPDNRTRVVEDNHNHYSRVYGPGEKQSQDLWDLVANRSHV 120  
  
Qy 120 KIHITLSNTHRQASRVLSFDPFPYGHPLRQITATTGCFIPMGDVIIHRMLTATQYVAPLM 179  
Db 121 KIHRISSSHRQASRVLSFDPFPYGHPLRQITATTGCFIPMGDMLHRMLTATQYVAPLM 180  
  
Qy 180 ANENPGYSDNVTYVFDNGTVFVQWDHVLQGHEDKGSFTFOALHHDGRIVFAYKEIP 239  
Db 181 ANFNPGYSDNVTYVFDNGTVFVQWDHVLQDREDRGSFTFOALHHDGRIVFAYKEIP 240  
  
Qy 240 MSVPFESSQHPVKTGLSDAFMILNPSDPVPESSRRSIFFYHRIELDPSKVTSMASVEFT 299  
Db 241 MAVLDISSAQHPVKAGLSDAFMLNPSPEVPESSQRTIFFYHRLVDELDSKITTSAVEFT 300  
  
Qy 300 PLPTCLHRSQCDACMSDLTNCNCHVLQRCSSGFDRYRQEWMDYCAQAEGRMCEDF 359  
Db 301 PLPTCLHQSCDTCVSSNLTFNCNCHVLQRCSSGFDRYRQEWLTYGCAQAEKTCEDF 360  
  
Qy 360 QDEHDSASPTSPYDGLTTTSSSLFIDSLTDEDTKLNPNVAGDGLONNLSPTKG 419  
Db 361 QDDSHYSASPOSSFPFNGD-STSSSLFIDSLTDEDTKLNPNVAGDGLPDHSPSKG 419  
  
Qy 420 TPVHLGTIVGIVLAVLLVAAILAGIYINGHPTNSAALFFIERRPHWPAMKFRSHPDHS 479  
Db 420 PPVHLGTIVGIVLAVLLVAAILAGIYISGHPNSNALFFIERRPHWPAMKFRSHPDHS 479  
  
Qy 480 TYAEVPSGHEKEGFMAEQ 500  
Db 480 TYTEVPSGHEKEGFMVEQ 500

RESULT 11

ABB90729 standard; protein; 500 AA.

ABB90729;  
30-MAY-2002 (first entry)  
Mouse Tumour Endothelial Marker polypeptide SEQ ID NO 192.

Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic;  
normal endothelial marker; pan-endothelial marker; immunostimulant;  
antiangiogenic; tumour; neoangiogenesis; vascularised tumour;  
polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;  
psoriasis.

Mus musculus.  
WO200210217-A2.

07-FEB-2002.

01-AUG-2001; 2001WO-US024031.

02-AUG-2000; 2000US-0222599P.

11-AUG-2000; 2000US-0224360P.

11-APR-2001; 2001US-0282850P.

(UYJO ) UNIV JOHNS HOPKINS.

St Croix B, Kinzler KW, Vogelstein B;

WPI; 2002-291856/33.

An isolated molecule comprising an antibody variable region which  
specifically binds to an extracellular domain of a tumor endothelial  
marker (TEM) protein, useful for inhibiting tumor growth.

Disclosure; Page 146-147; 331pp; English.

The invention relates to an isolated molecule comprising an antibody  
variable region which specifically binds to an extracellular domain of a  
tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740,  
ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM  
proteins have cytostatic, immunostimulant and antiangiogenic activity.  
They are useful for inhibiting tumour growth, neoangiogenesis in subjects  
bearing a vascularised tumour, polycystic kidney disease, diabetic  
retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM  
genes and the encoded proteins (ABL92075-ABL92141 and ABB90721-ABB90789)  
are disclosed, as are marker oligonucleotide sequences: tumour  
endothelial markers (TEM) ABL91996-ABL92041 and ABL92143-ABL92191; normal  
endothelial markers (NEM) ABL92042-ABL92074; and pan-endothelial markers  
(PEM) ABL91903-ABL91995

Sequence 500 AA;

Query Match 82.1%; Score 2209; DB 5; Length 500;

Best Local Similarity 81.6%; Pred. No. 6.7e-203;

Matches 409; Conservative 46; Mismatches 44; Indels 2; Gaps 2;

1 MRGLWLL-L-VLVLEAARALSPQAGHDEGPGSGWAAGTVRCGNRRARSPGHVSEPD 59

1 MRAQLWLLQLLLKGAARALSPATPAGHNEQDQSAWTAKTTRQGSRRPRSPQAVLKP 60

60 RTQLSQDLGGGTGLAMDTLPDNRTRVVEDNHNHYSRLYGPSEPHSRLWVDVAENRSQV 119

61 KTQLSQDLGGGSLAIDLTPDNRTRVVEDNHNHYSRVYGPGEKQSQDLWDLVANRSHV 120

120 KIHITLSNTHRQASRVLSFDPFPYGHPLRQITATTGCFIPMGDVIIHRMLTATQYVAPLM 179

121 KIHRISSSHRQASRVLSFDPFPYGHPLRQITATTGCFIPMGDMLHRMLTATQYVAPLM 180







Db 121 VYFDNGTVFVQWDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHP 180  
 Qy 252 VKTGLSDAFMLNPSDPVPSERRRSIFEYHRIELDPKSVTSMASAVEFTPLPTCLQHRSCD 311  
 Db 181 VKTGLSDAFMLNPSDPVPSERRRSIFEYHRIELDPKSVTSMASAVEFTPLPTCLQHRSCD 240  
 Qy 312 ACMSSDLTFNCWCHVLQRCSSGDFDRYQEW-MDYGCAQAEGRMCEDFQD-----ED 363  
 Db 241 ACMSSDLTFNCWCHVLQRCSSGDFDRYQEW-MDYGCAQAEGRMCEDFQD-----QDVRGLPGMRT 294  
 Qy 364 HDSASPDTSFSPYDGLTTSSSLFIDSLTTEDDTKLNYPAGGDLQNNLSPKTKGTPVH 423  
 Db 295 TTSASPDTSFSPYDGLTTSSSLFIDSLTTEDDTKLNYPAGGDLQNNLSPKTKGTPVH 354  
 Qy 424 LGTIVGIVLAVLLVAAILAGIYINGHPTSNAAFFIERRPHWPAMKFRSHPDHSTYAE 483  
 Db 355 LGTIVGIVLAVLLVAAILAGIYINGHPTSNAAFFIERRPHWPAMKFRSHPDHSTYAE 414  
 Qy 484 VEPGHEKEGFMABQC 500  
 Db 415 VEPGHEKEGFMABQC 431

## RESULT 15

AB001434  
 ID AB001434 standard; protein; 431 AA.

XX AC AB001434;

DT 07-AUG-2003 (first entry)

XX DE Human tumour endothelial marker 7 precursor protein.

XX KW Human; Gene therapy; stem cell inducer; osteoporosis; regeneration;  
 KW stem cell growth factor-like activity; leukaemia; haemophilia; allergy;  
 KW Parkinson's disease; Huntington's disease; amyotrophic lateral sclerosis;  
 KW autoimmune disease; multiple sclerosis; systemic lupus erythematosus;  
 KW graft-versus-host disease; degenerative disease; Alzheimer's disease;  
 KW osteoarthritis; anaemia; tendonitis; carpal tunnel syndrome; cancer;  
 KW tumour endothelial marker 7 precursor.

XX OS Homo sapiens.

XX PN US2003022825-A1.

XX PD 30-JAN-2003.

XX PF 24-JUL-2001; 2001US-00912935.

XX PR 23-DEC-2000; 2000WO-US035260.

XX PA (NISH/) NISHIKAWA M.

XX PA (LABA/) LABAT I.

XX PA (DRMA/) DRMANAC R T.

XX PA (TANG/) TANG Y T.

XX PA (CHAO/) CHAO C.

XX PI Nishikawa M, Labat I, Drmanac RT, Tang YT, Chao C;

XX DR WPI; 2003-456302/43.

XX PT New stem cell growth factor-like polypeptides and polynucleotides, useful  
 for treating e.g. leukemia, hemophilia, osteoporosis, osteoarthritis,  
 graft-versus-host disease, cancers, Alzheimer's disease, Huntington's  
 disease.

XX PS Example 4; Fig 2; 98pp; English.

XX CC The invention relates to a new isolated polypeptide, which has stem cell  
 growth factor-like activity. The new polypeptide, the polynucleotide  
 encoding this polypeptide, or the agonist of the polypeptide are useful  
 for treating a subject in need of enhanced activity or expression of stem  
 cell growth factor-like polypeptide. The antagonist of the polypeptide or

CC the polynucleotide is useful for treating a subject in need to inhibit  
 the activity or expression of stem cell growth factor-like polypeptide.  
 CC The new polypeptide or polynucleotide is particularly useful for inducing  
 differentiation of embryonic and adult stem cells to give rise to  
 CC different cell types. In particular, the polypeptide or polynucleotide is  
 CC useful for treating leukaemia, haemophilia, osteoporosis, osteoarthritis,  
 CC anaemia, tendonitis, carpal tunnel syndrome, autoimmune diseases (e.g.  
 CC multiple sclerosis, systemic lupus erythematosus, graft-versus-host  
 CC disease or allergies), cancers or degenerative diseases (e.g. Alzheimer's  
 CC disease, Parkinson's disease, Huntington's disease or amyotrophic lateral  
 CC sclerosis) or for generating new tissues and organs that may aid patients  
 CC in need of transplanted tissues. The polynucleotide may also be used in  
 CC gene therapy for the treatment of these diseases. The new polypeptide or  
 CC polynucleotide is also useful in diagnostic or research methods. The  
 CC present sequence represents the human tumour endothelial marker 7  
 CC precursor protein

XX SQ Sequence 431 AA;

Query Match 81.2%; Score 2185; DB 6; Length 431;  
 Best Local Similarity 95.2%; Pred. No. 1.1e-200;  
 Matches 416; Conservative 0; Mismatches 7; Indels 14; Gaps 3;

Qy 72 LAMDTLPDNRTRVVEDNHSYVSRLYGSPSPHSRELWVDVAENRSQVKHTILSNTHRQ 131  
 Db 1 LAMDTLPDNRTRVVEDNHSYVSRLYGSPSPHSRELWVDVAENRSQVKHTILSNTHRQ 60  
 Qy 132 ASRVLSFDPPFYGHPLRQITATGGFIFMGDVTHRMLTATQYVAPLMANFNPQYSDNST 191  
 Db 61 ASRVLSFDPPFYGHPLRQITATGGFIFMGDVTHRMLTATQYVAPLMANFNPQYSDNST 120  
 Qy 192 VYFDNGTVFVQWDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHP 251  
 Db 121 VYFDNGTVFVQWDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHP 180  
 Qy 252 VKTGLSDAFMLNPSDPVPSERRRSIFEYHRIELDPKSVTSMASAVEFTPLPTCLQHRSCD 311  
 Db 181 VKTGLSDAFMLNPSDPVPSERRRSIFEYHRIELDPKSVTSMASAVEFTPLPTCLQHRSCD 240  
 Qy 312 ACMSSDLTFNCWCHVLQRCSSGDFDRYQEW-MDYGCAQAEGRMCEDFQD-----ED 363  
 Db 241 ACMSSDLTFNCWCHVLQRCSSGDFDRYQEW-MDYGCAQAEGRMCEDFQD-----QDVRGLPGMRT 294  
 Qy 364 HDSASPDTSFSPYDGLTTSSSLFIDSLTTEDDTKLNYPAGGDLQNNLSPKTKGTPVH 423  
 Db 295 TTSASPDTSFSPYDGLTTSSSLFIDSLTTEDDTKLNYPAGGDLQNNLSPKTKGTPVH 354  
 Qy 424 LGTIVGIVLAVLLVAAILAGIYINGHPTSNAAFFIERRPHWPAMKFRSHPDHSTYAE 483  
 Db 355 LGTIVGIVLAVLLVAAILAGIYINGHPTSNAAFFIERRPHWPAMKFRSHPDHSTYAE 414  
 Qy 484 VEPGHEKEGFMABQC 500  
 Db 415 VEPGHEKEGFMABQC 431

Search completed: January 28, 2005, 22:05:06  
 Job time : 160.818 secs

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OM protein - protein search, using sw model

Run on: January 28, 2005, 21:59:20 ; Search time 17.7655 Seconds  
(without alignments)  
1321.880 Million cell updates/sec

Title: US-09-918-715-230\_COPY\_280\_344

Perfect score: 370

Sequence: 1 YHRIEIDPSKVTMSAVEFT.....CHVLQRCSSGFDYRQEWMD 65

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1608061 seqs, 361289386 residues

Total number of hits satisfying chosen parameters: 1608061

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	370	100.0	488	17	US-10-357-819-4
2	370	100.0	500	10	US-09-918-715-230
3	370	100.0	500	15	US-10-435-696-79
4	370	100.0	500	17	US-10-474-794-230
5	370	100.0	500	17	US-10-357-819-2
6	370	100.0	1002	10	US-09-918-715-179
7	370	100.0	1002	17	US-10-474-794-179
8	359	97.0	431	14	US-09-912-935-36
9	359	97.0	431	14	US-10-168-365-36
10	359	97.0	502	14	US-10-156-487A-5
11	325	87.8	500	10	US-09-918-715-192
12	325	87.8	500	10	US-09-918-715-297
13	325	87.8	500	14	US-10-156-487A-6

14	325	87.8	500	17	US-10-474-794-192
15	325	87.8	500	17	US-10-474-794-297
16	264	71.4	530	10	US-09-918-715-193
17	264	71.4	530	10	US-09-918-715-299
18	264	71.4	530	10	US-09-912-935-38
19	264	71.4	530	14	US-10-156-487A-2
20	264	71.4	530	14	US-10-281-478-12
21	264	71.4	530	17	US-10-474-794-193
22	264	71.4	530	17	US-10-474-794-299
23	264	71.4	530	17	US-10-487-421-2
24	263	71.1	392	10	US-09-912-935-23
25	263	71.1	392	10	US-09-912-935-25
26	263	71.1	392	14	US-10-168-365-23
27	263	71.1	392	14	US-10-168-365-25
28	263	71.1	425	10	US-09-912-935-35
29	263	71.1	425	14	US-10-168-365-35
30	263	71.1	449	10	US-09-912-935-34
31	263	71.1	449	14	US-10-168-365-34
32	263	71.1	499	10	US-09-912-935-31
33	263	71.1	499	14	US-10-168-365-31
34	263	71.1	529	10	US-09-918-715-189
35	263	71.1	529	10	US-09-918-715-200
36	263	71.1	529	10	US-09-912-935-28
37	263	71.1	529	10	US-09-912-935-40
38	263	71.1	529	13	US-10-052-586-472
39	263	71.1	529	13	US-10-066-500-128
40	263	71.1	529	14	US-10-174-590-472
41	263	71.1	529	14	US-10-176-758-472
42	263	71.1	529	14	US-10-175-737-472
43	263	71.1	529	14	US-10-174-581-472
44	263	71.1	529	14	US-10-176-483-472
45	263	71.1	529	14	US-10-176-749-472

ALIGNMENTS

RESULT 1

- US-10-357-819-4
- Sequence 4, Application US/10357819
- Publication No. US20040259774A1
- GENERAL INFORMATION:
- APPLICANT: Alvarez, Enrique
- APPLICANT: Edinger, Shlomit R.
- APPLICANT: Gangolli, Esha A.
- APPLICANT: Gerlach, Valerie L.
- APPLICANT: Gorman, Linda
- APPLICANT: Guo, Xiaojia
- APPLICANT: Ji, Weizhen
- APPLICANT: Kekuda, Ramesh
- APPLICANT: Li, Li
- APPLICANT: Miller, Charles E.
- APPLICANT: Padigaru, Muralidhara
- APPLICANT: Patturajan, Meera
- APPLICANT: Rastelli, Luca
- APPLICANT: Rieger, Daniel K.
- APPLICANT: Shenoy, Suresh G.
- APPLICANT: Shimkets, Richard A.
- APPLICANT: Sytek, Kimberly A.
- APPLICANT: Zhong, Mei
- TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
- FILE REFERENCE: 21402-538A
- CURRENT APPLICATION NUMBER: US/10/357,819
- CURRENT FILING DATE: 2003-02-03
- PRIOR APPLICATION NUMBER: 09/520,781
- PRIOR FILING DATE: 2000-03-08
- PRIOR APPLICATION NUMBER: 09/584,411
- PRIOR FILING DATE: 2000-05-31
- PRIOR APPLICATION NUMBER: 09/783,436
- PRIOR FILING DATE: 2001-02-14
- PRIOR APPLICATION NUMBER: 10/085,198
- PRIOR FILING DATE: 2002-02-25
- PRIOR APPLICATION NUMBER: 60/353,301

Sequence 192, App
Sequence 297, App
Sequence 193, App
Sequence 299, App
Sequence 38, Appli
Sequence 2, Appli
Sequence 12, Appl
Sequence 193, App
Sequence 299, App
Sequence 2, Appli
Sequence 23, Appl
Sequence 25, Appl
Sequence 25, Appl
Sequence 35, Appl
Sequence 35, Appl
Sequence 34, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 189, App
Sequence 200, App
Sequence 28, Appl
Sequence 40, Appl
Sequence 472, App
Sequence 128, App
Sequence 472, App
Sequence 472, App
Sequence 472, App
Sequence 472, App
Sequence 472, App



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RESULT 5
US-10-357-819-2
; Sequence 2, Application US/10357819
; Publication No. US20040259774A1
; GENERAL INFORMATION:
; APPLICANT: Alvarez, Enrique
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Gorman, Linda
; APPLICANT: Guo, Xiaojia
; APPLICANT: Ji, Weizhen
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Li, Li
; APPLICANT: Miller, Charles E.
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Rastelli, Luca
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Shenov, Suresh G.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-538A
; CURRENT APPLICATION NUMBER: US/10/357,819
; PRIOR FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 09/584,411
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 09/783,436
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 10/085,198
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 60/353,301
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 60/355,099
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: 60/356,424
; PRIOR FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: 60/358,239
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: 60/358,608
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/359,367
; PRIOR FILING DATE: 2002-02-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 2
; LENGTH: 500
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-357-819-2

Query Match 100.0%; Score 370; DB 17; Length 500;
Best Local Similarity 100.0%; Pred. No. 1.9e-36;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YHRIELDPKVTSMASAVEFTPLPTCLOHRS CDACMSSDLTFNC SWCHVLQRCSSGFDYR 60
Db 280 YHRIELDPKVTSMASAVEFTPLPTCLOHRS CDACMSSDLTFNC SWCHVLQRCSSGFDYR 339

Qy 61 QEWMD 65
Db 340 QEWMD 344

RESULT 6
US-09-918-715-179
; Sequence 179, Application US/09918715
; Publication No. US20030017157A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/09/918,715
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 179
; LENGTH: 1002
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-918-715-179

Query Match 100.0%; Score 370; DB 10; Length 1002;
Best Local Similarity 100.0%; Pred. No. 3.9e-36;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YHRIELDPKVTSMASAVEFTPLPTCLOHRS CDACMSSDLTFNC SWCHVLQRCSSGFDYR 60
Db 782 YHRIELDPKVTSMASAVEFTPLPTCLOHRS CDACMSSDLTFNC SWCHVLQRCSSGFDYR 841

Qy 61 QEWMD 65
Db 842 QEWMD 846

RESULT 7
US-10-474-794-179
; Sequence 179, Application US/10474794
; Publication No. US20040213793A1
; GENERAL INFORMATION:
; APPLICANT: Carson-Walter, Eleanor
; APPLICANT: St. Croix, Brad
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00179
; CURRENT APPLICATION NUMBER: US/10/474,794
; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 60/308,829
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 359
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 179
; LENGTH: 1002
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-474-794-179

Query Match 100.0%; Score 370; DB 17; Length 1002;
Best Local Similarity 100.0%; Pred. No. 3.9e-36;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YHRIELDPKVTSMASAVEFTPLPTCLOHRS CDACMSSDLTFNC SWCHVLQRCSSGFDYR 60
Db 782 YHRIELDPKVTSMASAVEFTPLPTCLOHRS CDACMSSDLTFNC SWCHVLQRCSSGFDYR 841

Qy 61 QEWMD 65
Db 842 QEWMD 846
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RESULT 8
US-09-912-935-36
; Sequence 36, Application US/09912935
; Publication No. US20030022825A1
; GENERAL INFORMATION:
; APPLICANT: Nishikawa, Mitsuo et al.
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
; FILE REFERENCE: 32066/37483
; CURRENT APPLICATION NUMBER: US/09/912,935
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: PCT/US00/35260
; PRIOR FILING DATE: 2000-12-23
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 36
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-912-935-36

Query Match          97.0%; Score 359; DB 10; Length 431;
Best Local Similarity 100.0%; Pred. No. 3.5e-35;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YHRIELDPKVTSMASAVEFTPLPTCLOHRSCDACMSSDLTFCNCWCHVLQRCSSGFDYR 60
Db 209 YHRIELDPKVTSMASAVEFTPLPTCLOHRSCDACMSSDLTFCNCWCHVLQRCSSGFDYR 268

Qy 61 QEW 63
Db 269 QEW 271

RESULT 9
US-10-168-365-36
; Sequence 36, Application US/10168365
; Publication No. US20030211987A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Childs, John
; APPLICANT: Chao, Cheng-Chi
; APPLICANT: Drmanac, Radoje T
; APPLICANT: Mize, Nancy
; APPLICANT: Lee, Juh1
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
; FILE REFERENCE: 30266/37630
; CURRENT APPLICATION NUMBER: US/10/168,365
; CURRENT FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 36
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-168-365-36

Query Match          97.0%; Score 359; DB 14; Length 431;
Best Local Similarity 100.0%; Pred. No. 3.5e-35;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YHRIELDPKVTSMASAVEFTPLPTCLOHRSCDACMSSDLTFCNCWCHVLQRCSSGFDYR 60
Db 209 YHRIELDPKVTSMASAVEFTPLPTCLOHRSCDACMSSDLTFCNCWCHVLQRCSSGFDYR 268

Qy 61 QEW 63
Db 269 QEW 271

RESULT 10
US-10-156-487A-5
; Sequence 5, Application US/10156487A
; Publication No. US20030092025A1
; GENERAL INFORMATION:
; APPLICANT: Juan, Todd
; APPLICANT: Bass, Michael B.
; APPLICANT: Oliner, John
; TITLE OF INVENTION: Tumor Endothelial Marker 7a Molecules and Uses Thereof
; FILE REFERENCE: 01-072-A
; CURRENT APPLICATION NUMBER: US/10/156,487A
; CURRENT FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: 60/293,852
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-156-487A-5

Query Match          97.0%; Score 359; DB 14; Length 502;
Best Local Similarity 100.0%; Pred. No. 4.1e-35;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YHRIELDPKVTSMASAVEFTPLPTCLOHRSCDACMSSDLTFCNCWCHVLQRCSSGFDYR 60
Db 280 YHRIELDPKVTSMASAVEFTPLPTCLOHRSCDACMSSDLTFCNCWCHVLQRCSSGFDYR 339

Qy 61 QEW 63
Db 340 QEW 342

RESULT 11
US-09-918-715-192
; Sequence 192, Application US/09918715
; Publication No. US20030017157A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/09/918,715
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 192
; LENGTH: 500
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-918-715-192

Query Match          87.8%; Score 325; DB 10; Length 500;
Best Local Similarity 84.4%; Pred. No. 5.7e-31;
Matches 54; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YHRIELDPKVTSMASAVEFTPLPTCLOHRSCDACMSSDLTFCNCWCHVLQRCSSGFDYR 60
Db 281 YHRIELDPKVTSMASAVEFTPLPTCLOHRSCDACMSSDLTFCNCWCHVLQRCSSGFDYR 340

Qy 61 QEW 64
Db 340 QEW 342
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Db 341 QEWL 344

## RESULT 12

US-09-918-715-297  
; Sequence 297, Application US/09918715  
; Publication No. US20030017157A1  
; GENERAL INFORMATION:

; APPLICANT: Bert Vogelstein  
; APPLICANT: Brad St. Croix  
; APPLICANT: Kenneth Kinzler  
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS  
; FILE REFERENCE: 1107.00134

; CURRENT APPLICATION NUMBER: US/09/918,715  
; CURRENT FILING DATE: 2001-08-01

; PRIOR FILING DATE: 2001-08-01  
; PRIOR FILING DATE: 2000-08-02

; PRIOR APPLICATION NUMBER: 60/224,360  
; PRIOR FILING DATE: 2000-08-11

; PRIOR APPLICATION NUMBER: 60/282,850  
; PRIOR FILING DATE: 2000-04-11

; NUMBER OF SEQ ID NOS: 358  
; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 297  
; LENGTH: 500

; TYPE: PRT  
; ORGANISM: Mouse

US-09-918-715-297

Query Match 87.8%; Score 325; DB 10; Length 500;  
Best Local Similarity 84.4%; Pred. No. 5.7e-31;

Matches 54; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YHRIELPSKVTMSAVEFTPLPTCLOHRSDCACMSSDLTFCNSCHVLCRCSSGFDYR 60

Db 281 YHVELSSKITTTTSAVEFTPLPTCLOHRSDCACMSSDLTFCNSCHVLCRCSSGFDYR 340

Qy 61 QEWM 64

Db 341 QEWL 344

## RESULT 13

US-10-156-487A-6  
; Sequence 6, Application US/10156487A  
; Publication No. US20030092025A1  
; GENERAL INFORMATION:

; APPLICANT: Juan, Todd  
; APPLICANT: Bass, Michael B.  
; APPLICANT: Oliner, John

; TITLE OF INVENTION: Tumor Endothelial Marker 7a Molecules and Uses Thereof  
; FILE REFERENCE: 01-072-A

; CURRENT APPLICATION NUMBER: US/10/156,487A  
; CURRENT FILING DATE: 2002-09-10

; PRIOR APPLICATION NUMBER: 60/293,852  
; PRIOR FILING DATE: 2001-05-25

; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 6  
; LENGTH: 500

; TYPE: PRT  
; ORGANISM: Mus musculus

US-10-156-487A-6

Query Match 87.8%; Score 325; DB 14; Length 500;  
Best Local Similarity 84.4%; Pred. No. 5.7e-31;

Matches 54; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YHRIELPSKVTMSAVEFTPLPTCLOHRSDCACMSSDLTFCNSCHVLCRCSSGFDYR 60

Db 281 YHVELSSKITTTTSAVEFTPLPTCLOHRSDCACMSSDLTFCNSCHVLCRCSSGFDYR 340

Qy 61 QEWM 64

Db 341 QEWL 344

## RESULT 14

US-10-474-794-192  
; Sequence 192, Application US/10474794  
; Publication No. US20040213793A1  
; GENERAL INFORMATION:

; APPLICANT: Carson-Walter, Eleanor  
; APPLICANT: St. Croix, Brad

; APPLICANT: Vogelstein, Bert  
; APPLICANT: Kinzler, Kenneth

; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS  
; FILE REFERENCE: 1107.00179

; CURRENT APPLICATION NUMBER: US/10/474,794  
; CURRENT FILING DATE: 2003-10-14

; PRIOR APPLICATION NUMBER: 60/282,850  
; PRIOR FILING DATE: 2001-04-11

; PRIOR APPLICATION NUMBER: 60/308,829  
; PRIOR FILING DATE: 2001-08-01

; NUMBER OF SEQ ID NOS: 359  
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 192  
; LENGTH: 500

; TYPE: PRT  
; ORGANISM: Mus musculus

US-10-474-794-192

Query Match 87.8%; Score 325; DB 17; Length 500;  
Best Local Similarity 84.4%; Pred. No. 5.7e-31;

Matches 54; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YHRIELPSKVTMSAVEFTPLPTCLOHRSDCACMSSDLTFCNSCHVLCRCSSGFDYR 60

Db 281 YHVELSSKITTTTSAVEFTPLPTCLOHRSDCACMSSDLTFCNSCHVLCRCSSGFDYR 340

Qy 61 QEWM 64

Db 341 QEWL 344

## RESULT 15

US-10-474-794-297  
; Sequence 297, Application US/10474794  
; Publication No. US20040213793A1  
; GENERAL INFORMATION:

; APPLICANT: Carson-Walter, Eleanor  
; APPLICANT: St. Croix, Brad

; APPLICANT: Vogelstein, Bert  
; APPLICANT: Kinzler, Kenneth

; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS  
; FILE REFERENCE: 1107.00179

; CURRENT APPLICATION NUMBER: US/10/474,794  
; CURRENT FILING DATE: 2003-10-14

; PRIOR APPLICATION NUMBER: 60/282,850  
; PRIOR FILING DATE: 2001-04-11

; PRIOR APPLICATION NUMBER: 60/308,829  
; PRIOR FILING DATE: 2001-08-01

; NUMBER OF SEQ ID NOS: 359  
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 297  
; LENGTH: 500

; TYPE: PRT  
; ORGANISM: Mouse

US-10-474-794-297

Query Match 87.8%; Score 325; DB 17; Length 500;  
Best Local Similarity 84.4%; Pred. No. 5.7e-31;

Matches 54; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YHRIELPSKVTMSAVEFTPLPTCLOHRSDCACMSSDLTFCNSCHVLCRCSSGFDYR 60

Db 281 YHRVELDSSKITTTSAVEFTPLPTCLOHQSCDTCVSSNLTENC5WCHVJQRCSSGFDYR 340  
Qy 61 QEWL 64  
Db 341 QEWL 344

Search completed: January 28, 2005, 22:19:19  
Job time : 18.7655 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 28, 2005, 21:55:58 ; Search time 28.3934 Seconds  
(without alignments)  
1389.370 Million cell updates/sec

Title: US-09-918-715-230\_COPY\_18\_427  
Perfect score: 2218  
Sequence: 1 AUSPPQAGHDEGFGSGWAA.....GLQNNLSPTKTPVHLGTI 410

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	603	27.2	476	2 T19786	hypothetical prote
2	126	5.7	1161	1 S31213	nidogen precursor
3	115.5	5.2	1568	2 T09074	semaphorin recepto
4	101.5	4.6	743	2 T09173	EH domain protein
5	100.5	4.5	979	2 C86446	probable cellulose
6	99	4.5	535	2 S18606	phosphoenolpyruvat
7	99	4.5	1133	2 T12529	hypothetical prote
8	98	4.4	1502	2 S45429	probable membrane
9	96.5	4.4	397	2 S33415	corticosteroid-bin
10	95.5	4.3	679	2 T19703	hypothetical prote
11	95.5	4.3	2120	2 T30243	alpha tectorin - c
12	95	4.3	708	2 T83136	NEDD-4 ORF - mouse
13	94	4.2	774	2 JC7265	neprilysin (EC 3.4
14	93.5	4.2	887	2 S70642	ubiquitin ligase N
15	93.5	4.2	979	1 JC2349	protein-tyrosine-p
16	93.5	4.2	996	2 T48721	PIP 35 protein - m
17	93.5	4.2	1977	2 S54771	sodium channel alp
18	93	4.2	491	2 AG3506	phosphoenolpyruvat
19	93	4.2	1085	2 S55352	IFH1 protein - yea
20	91.5	4.1	614	2 A98241	hypothetical prote
21	91.5	4.1	614	2 F86088	hypothetical prote
22	91.5	4.1	810	1 F2WMB8	2a protein - broad
23	91.5	4.1	1042	2 A57534	mucin 5AC (clone L
24	90.5	4.1	332	2 JN0067	pregnancy-specific
25	90	4.1	561	2 AD2561	phosphoenolpyruvat
26	90	4.1	561	2 B97363	phosphoenolpyruvat
27	90	4.1	798	2 T25104	hypothetical prote
28	90	4.1	1176	2 T58345	protein tyrosine p
29	90	4.1	1179	2 T05673	hypothetical prote

30	89.5	4.0	424	2 A34595	pregnancy-specific
31	89.5	4.0	1840	1 CHRTM1	sodium channel pro
32	89	4.0	673	2 T31610	hypothetical prote
33	89	4.0	934	2 T15063	hypothetical prote
34	89	4.0	946	2 A84133	hypothetical prote
35	89	4.0	2155	2 T30197	alpha tectorin - m
36	88.5	4.0	441	2 JC7653	pectate lyase (EC
37	88.5	4.0	538	2 T49849	related to DRPLA p
38	88.5	4.0	1175	2 S51005	protein-tyrosine-p
39	88.5	4.0	4957	2 T03455	ALR protein - huma
40	88.5	4.0	5262	2 T03454	ALR protein - huma
41	88	4.0	528	2 S42510	Rag-2 protein - ch
42	88	4.0	653	2 T03102	semaphorin homolog
43	88	4.0	1123	2 T30880	dyein heavy chain
44	88	4.0	1349	2 S51471	killer toxin insen
45	88	4.0	3343	2 S44887	ZK112.7 protein -

ALIGNMENTS

RESULT 1

T19786  
hypothetical protein C36E8.3 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T19786  
R;Wilkinson, J.; Barlow, K.  
submitted to the EMBL Data Library, August 1994  
A;Reference number: Z19177  
A;Accession: T19786  
A;Status: preliminary; translated from GB/EMBL/DBDJ  
A;Molecule type: DNA  
A;Residues: 1-476 <WIL>  
A;Cross-references: UNIPROT:Q18500; EMBL:Z35597; PIDN:CAA84646.1; GSPDB:GN00021; CESP:C3  
A;Experimental source: clone C36E8  
C;Genetics:  
A;Gene: CESP:C36E8.3  
A;Map position: 3  
A;Introns: 23/1; 101/3; 152/3; 206/3; 235/1; 255/3; 320/1; 445/2  
C;Superfamily: Caenorhabditis elegans hypothetical protein C36E8.3

Query Match 27.2%; Score 603; DB 2; Length 476;

Best Local Similarity 35.8%; Pred. No. 4.5e-42;

Matches 144; Conservative 64; Mismatches 156; Indels 38; Gaps 14;

Qy	29	RRRESGHSVSEPDRTOLS-----ODLGGGTFLAMDTLPDNRTRVVDNHSYVSRLYGPS	83
Db	62	RTAAAP-----IPKSLASQDEEDIDPATATIP--PDVEKNDMDHQYQAEYFGVD	115
Qy	84	EPHSRELWVDVAEANSQVKI-----HTILNTHRQASRVVLSFPDFPYGHPRLQITATG	139
Db	116	GETLKKYWINVEQPMKKPAVGNTHSPLLSQSYRRAVGARLQPKFPFVGHGMSNLTIATG	175
Qy	140	GFPMGVIIHRMLTATQYVAPLAFMANFPGYSDNSTVYFNGTIVVQWHDHYLQGHEDK	199
Db	176	GFYIGDHSNHLAATQYIAPLAFMANFHT-YLNNSNIYVADGDELGVVVEWRNVQLKEDKE	234
Qy	200	GSFTFOALHHDGRIVEYAYKEIPMSVPEISSQHPVKTGSLDAPMILN--PSPDVPESRR	257
Db	235	HSFTFTQILHKGNDIVFIYKDPYDINISDANHPVKLGISDAYMFRHNLHQAAPV---K	291
Qy	258	RSIFEXYHRIELDSKVTSMGSAVEFTPLPTCLQHRSCDACMSSDLT-FNCSCHVLQR---	313
Db	292	RVIVEXYHRIEIAQKIVSNVTWILKAQPTCISPDCTCTNATLPHENCLCHAKKSHGG	351
Qy	314	--CS--SGFDRYRQEWMDYCAQAEGRMCE-DQDEHDHSAS-PDTSFSFYDGLTTTS	367
Db	352	PFCTDEAGLHRRQRHWFEGNICYQSKALYCDADDEDEYDEEDYPKSQLMPNGGH---TV	408
Qy	368	SSLFIDSLTITTEDDTKLNIPYAGGDLQNNLSPK-----TKGTPV	405
Db	409	LPLDADKKKTKDITTSSEDSDEWKGKKKEPKGGVATTATPV	450



```
Db 180 SPADTPPTSAITMHPASVODQTTVRTVASAATANEIRQSSSYEDPW-----KITDE- 232
Qy 139 GGFIFMGDVHRLMTATQY--VAPLMANFNPGYSDNSTVVYFDNGTVFVQWDMHYV-LQG 195
Db 233 -----QRYVYVQFKTIQDLNGFIQF---SAAKEFTYKSKPILELSHWELSD 279
Qy 196 WEDKGSFT---FOAALHHDGRIVFAYK---BIPMSVPEISSQHPVKTGLSDAFMILNPS 249
Db 280 FDKDGLALTDFECAAFFH---LVARKNGYDLPEKLP-----SLMPKLIDLEDS 325
Qy 250 PDVPESSRRRSIFEYHRIELDPKSKYTSMSAVEFTPLPTCLOHRSCDACWSSDLTFCNSWCH 309
Db 326 ADVGEQFGEVGYSGPAEAPPSPSPSL-----NQTWPE 361
Qy 310 VLQRCSSGFDYRQEWMDYGAQBAEGRMCDFOEDHDSASPDS----- 355
Db 362 LNQS-----SQWETFS-ERSSSQTLTQF-DSNIAPADPTAIVHPVPIRMTPSKI 411
Qy 356 -----FSPYDGLTTSSSLFIDSLTTEDTKLNP-----YAGDGLQNNLS 397
Db 412 HMQEMELKRTSSDHTNPTSPVLKPSDLSEENKINSVKPPSGNTVDGYSSSDSGPSPD-- 469
Qy 398 PKTXGTPV-----HLGT 409
Db 470 PEQIGSSVTRQSRHSGT 486

RESULT 5
C86446
probable cellulose synthase catalytic subunit [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: C86446
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: C86446
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-979 <STO>
A;Cross-references: UNIPROT:Q9FVR3; GB:AE005172; NID:g10801364; PIDN:AAG23436.1; GSPDB:G
C;Genetics:
A;Map position: 1

Query Match 4.5%; Score 100.5; DB 2; Length 979;
Best Local Similarity 21.1%; Pred. No. 6.1;
Matches 83; Conservative 47; Mismatches 155; Indels 109; Gaps 19;

Qy 4 PQPGAGHDEGPGCGAAKGTVRGNRRARESPGHVSEPDRTQLSQDL-----G 51
Db 359 PRPAL-----VAPKATWMSDGT--HWPGTWVSGPHRSGDHASVIQVLDDPDPGPVSGKG 413
Qy 52 GGTLLAMP-----TLPDNRTRVEDNHSYVRLYGPSPHRSRLWVDVAEANSRQVKIH 105
Db 414 GEGRALDLEGVDIIRLP-----MLVYVSREKRPYDHNKK-----AGAMNALVRAS 458
Qy 106 TILSNTRQASRVVLSDFEPYPGHPLRQITATGGFIPMGDVIHRMLTATQY----- 157
Db 459 AIMSND-----GPFILNLDCHYVNSRAF---RDGICFMMDHGDGRVSYVQFPORFEGID 510
Qy 158 VAPLMANFNPGYSD-----NSTVYV-FDNGTVFVQWDMHYVLOG 195
Db 511 PSDRYANKNTVFFDINLRALDGIQGPVMYGTGCLFRRTALYGFNPDPVFVVE----- 562
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```
Qy 196 WEDKGSFTFOAALHHDGRIVFAYKEIPMSV---PEISSQHP-----VKTGLSDAFMIL 246
Db 563 EEPGSGYCFP-----LIKKRSPATVASEPEYTTDEEDRFDIGLIRKQFGSSSMLV 612
Qy 247 NPSPDVPESRRRSIFEYH--RIELDPKSKVT--SMSAVEFTPLPTCLOHRSCDACWSSDLTF 303
Db 613 N-SVKVAEAFEGRPLATVHSSRLGPPGSLTGSRLKPLDFATVNEAVNIVSWYEDKTEWGF 671
Qy 304 NCSCWH--VLQRCSSGFDYRQEWMDYGAQBAE 335
Db 672 NVGMIYGSVTEVDVYTFGRMEHKGWRSFYCVTEPD 705

RESULT 6
S18606
phosphoenolpyruvate carboxykinase (ATP) (EC 4.1.1.49) - Rhizobium sp.
C;Species: Rhizobium sp.
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 27-Oct-2003
C;Accession: S18606
R;Osteras, M.; Finan, T.M.; Stanley, J.
Mol. Gen. Genet. 230, 257-269, 1991
A;Title: Site-directed mutagenesis and DNA sequence of pckA of Rhizobium NGR234, encodin
A;Reference number: S18606; MUID:92079905; PMID:1720862
A;Accession: S18606
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-535 <OST>
A;Cross-references: EMBL:X63291
C;Superfamily: phosphoenolpyruvate carboxykinase [ATP]
C;Keywords: carbon-carbon lyase; carboxy-lyase; nucleotide binding; P-loop
F;234-241/Region: nucleotide-binding motif A (P-loop)

Query Match 4.5%; Score 99; DB 2; Length 535;
Best Local Similarity 20.7%; Pred. No. 3.5;
Matches 59; Conservative 39; Mismatches 117; Indels 70; Gaps 12;

Qy 61 PDNRTRVVD-----NHSYVSRLYGPSPHRSRLWVDVAEANSRQVKIHTI-LSNTHR 113
Db 86 PENFERLRQDLAHAKGMSLYQDLVGAGSGK-----CVADARRHRIRHWSLFTRNLLI 140
Qy 114 QASRVVLS-----PDFP-FYGHF-----LRQITATGGFIFMGDVHVR 150
Db 141 RPPREGLASFLPKTIIDLPFSKANPERHGCGRGTIIACDLTKGLVLIGGTSYAGEMKKS 200
Qy 151 MLTATQTVAP-----LMANFNPGYSDNSTVYF-----DNGTVFVQWDMH 190
Db 201 VFTVNLVLLPNKAVPMHCSANVCPA---GDTAIFFGLSGTGKTLSDPNRTLIGDDEH 257
Qy 191 VYLOGWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHPVKTGLSDAFMILNPS 250
Db 258 ----GMSDKGVFNPEG-----GCYAKAIRLSEAAPEIFATRRFRFGTMENVVLDERRAP 308
Qy 251 DVPESSRRRSIFEYHRIELDPKSKYTSMSAVEFTPLPTCLOHRSCDA 295
Db 309 DFONG-----SLTENTRIAYPLDFIPNASETGTAPOQFRTIIMLTADA 350

RESULT 7
T12529
hypothetical protein DKFZp434p13.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004
C;Accession: T12529
R;Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, June 1999
A;Reference number: Z17524
A;Accession: T12529
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1133 <WAM>
A;Cross-references: UNIPROT:Q9UG37; EMBL:AL080145
A;Experimental source: adult testis; clone DKFZp434p13
C;Genetics:
```



```
Db 269 VVAALNREDTIDRWGKMLIP-RQMNLVTPKFSMSTYDLQVLADVGKDLFTNOSDFADT 327
Qy 253 PESRRRSIFEYHR--IELDPSKV 273
Db 328 TKDTPFLITLVHLKAMQLDEGNV 350

RESULT 10
T19703
hypothetical protein C34C12.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T19703
R;Kershaw, J.
submitted to the EMBL Data Library, December 1994
A;Reference number: Z19166
A;Accession: T19703
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-679 <WIL>
A;Cross-references: UNIPROT:Q09495; EMBL:Z46996; PIDN:CAA87102.1; GSPDB:GN00021; CESP:C3
A;Experimental source: clone C34C12
C;Genetics:
A;Gene: CESP:C34C12.2
A;Map position: 3
A;Introns: 5/3; 72/3; 125/3; 173/3; 511/3; 605/3

Query Match 4.3%; Score 95.5; DB 2; Length 679;
Best Local Similarity 24.4%; Pred. No. 9.6; Mismatches 31; Indels 65; Gaps 12;
Matches 65; Conservative 31;

Qy 34 SPGHVSFPDRTQLSQDLGGGTGLAMDTLPDNRTRVVEDNHSYVGRLYGSPSPHRELWVD 93
Db 372 SPG---PGRTQISDLQNTGEVRY-----VNSSKPFNFS-----SESNSRLKLI 414

Qy 94 VAEANRSQ---VKLHTILSNTHRQASRVLSFDPFPFGHPLRQITAT-----GGFIM 144
Db 415 PGYIKRPEFRYKPEGTSTASYKAQSGMSF-----LKTGSSATPENSCKSAHFDM 466

Qy 145 GDVTHRLMTATQYVAPLMAANNPGYSDNSTVVF-----DNGTVFVQWDHVLQGWEDK 199
Db 467 PDI-----SSTPYKSHVVVEDSNSSSTIGGFESKKNQAL-----GSQKS 510

Qy 200 GSFTFQAALHHDGRIVFAYKEIPMSVPEISSQHPVKTGLSDAFMILNPSDPVPSRRRS 259
Db 511 PMPDIATALHN----IFDSKEVQSSSTGSSAIPENSCKSDHF-----DMPDISSTLYRS 562

Qy 260 IFYVHRIELDPKVTSMASAVEFTPLP 285
Db 563 RVE--PISSSSSGSTSTSAPIYVPEK 586

RESULT 11
T30243
alpha tectorin - chicken
C;Species: Gallus gallus (chicken)
C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 09-Jul-2004
C;Accession: T30243
R;Coutinho, P.; Goodyear, R.G.; Legan, P.K.; Richardson, G.P.
Hear. Res. 130, 62-74, 1999
A;Title: Chick alpha tectorin : molecular cloning and expression during embryogenesis.
A;Reference number: 220783; MUID:99251817; PMID:10320099
A;Accession: T30243
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-2120 <COU>
A;Cross-references: UNIPROT:Q9YH85; EMBL:AJ012287; NID:e1361091; PIDN:CAAC
A;Note: non-collagenous protein only expressed in the inner ear

Query Match 4.3%; Score 95.5; DB 2; Length 2120;
Best Local Similarity 24.4%; Pred. No. 46; Mismatches 54; Conservative 28; Indels 72; Gaps 13;
```

```
Qy 115 ASRVLSFDPFPFGHPLRQITATGGFIFMGDVHR-----MLTATQYVAPL---MAN 164
Db 46 SSEIKLSVPFIFRSPRYTVVNNNGVISFNSLSVQFTPEAFPLADGRAFAVAFPGCDVAN 105
Qy 165 -----FNP---GYSNSTVVFEDN-----GTVFVQWDHVLQGWEDKGSF-- 202
Db 106 GIRGEIYYRESTNPGLGESSKDIRKFKOMASFSASVWFIWVEEQFYG-----GSSTT 161
Qy 203 ---TFQAALHHDG---RIVFAYKEIPMSVPEISSQHPVKTGL-----SDA 242
Db 162 PNTFQAVLITDGVSSFAIFNYQELSWTTGTASGD-PL-TGLGGVMAQAQFNGNINNF 219
Qy 243 FMIL-NPSPDPVESRR-----RSIFEYHRIELDPKSVT 274
Db 220 FSIPTGSRTPDIVNIEQTNNVNIPIGRWAFKIDGREIDPANLS 260

RESULT 12
I83196
NEDD-4 ORF - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 18-Aug-2000
C;Accession: I83196
R;Kumar, S.; Tomooka, Y.; Noda, M.
Biochem. Biophys. Res. Commun. 185, 1155-1161, 1992
A;Title: Identification of a set of genes with developmentally down-regulated expression
A;Reference number: I60167; MUID:92328780; PMID:1378265
A;Accession: I83196
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-708 <RES>
A;Cross-references: GB:D10714; NID:g220508; PID:g220509
C;Genetics:
A;Gene: NEDD-4
C;Superfamily: rat ubiquitin-protein ligase; protein kinase C 2 region homology; ubiquitin
F;40-77/Domain: WW repeat homology <WW1>
F;196-233/Domain: WW repeat homology <WW2>
F;251-288/Domain: WW repeat homology <WW3>
F;347-682/Domain: ubiquitin-protein ligase homology <UB1>

Query Match 4.3%; Score 95; DB 2; Length 708;
Best Local Similarity 19.3%; Pred. No. 11; Mismatches 150; Indels 180; Gaps 24;
Matches 91; Conservative 50;
```

```
Qy 5 QPGAG---HDEGPG---SGWAAKGTVRG---WNRARESPCHVSPD----- 42
Db 26 QPDAATHLPHPPSPPLPPGWEERQDVLGRYYVNHESRRRTQWKRPSPDDDLTDNDMD 85

Qy 43 -----RTQLSODLGGGTGLAMDTLPDNRTR-----VVEDNHSYVSR-LYGPSEP 85
Db 86 HSRELWVDVAEANRSQVKIHTILSNTHRQASRVLSFDF-----PFYGHPLRQITATGGF 141
Qy 138 H-----IDV-----QTH-----LAEFNTRLAVCGNPATSPQVTSNNH 170
Db 142 IFMGDVIHRLMTATQYVAPLMA---ANFNPGY-----SDNSTVVFQDNGTVFVQWDHVL 193
Qy 171 SSRGGSLOTCIFERQPTLPVLLPTSSGLPPGWEKQDDRGSRVYVDHNSK-TTWSKPTM 229
Db 194 Q-----GWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEI 228
Db 230 QDDPRSKI PAHLRGKTDSDNLGPLPPGWEER-----THTDGRVFFINHIKKTQWED 281
Qy 229 SSSQHPVKTGLSDAFMILNPSDPVPSR-RSIFEYHRIELDPKSVTSMASAVEFTPLPTC 287
Db 282 PRLQNVATG-----PAPYSRDYKRYKFFFRKLKKQ-----TDIPNK 320
Qy 288 LOHRSQCDACMSSDLTFNCSSWCHVLQRCSSGFDYRQSWMDYGCQAQEAECRMCEDFOBE-- 345
Db 321 PEMK-----LRRANILEDSTYR-IMGVSRADLLKARLWIEFDGEKG 360
```

```
Qy 346 -DHDSASP-----TSFSFYDGLDTTSSSLFIDSLTTEDDTKLNYPAG 388
      : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 361 LDYGGVAREWFLLISKEMFNYYG-----LFEYSATDNYTLQINPSG 403
      : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 13
neprilysin (EC 3.4.24.11) II - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 02-Sep-2000
C:Accession: JC7265
R:Tanja, O.; Facchinetti, P.; Rose, C.; Bonhomme, M.C.; Gros, C.; Schwartz, J.C.
Biochem. Biophys. Res. Commun. 271, 565-570, 2000
A>Title: Neprilysin II: A putative novel metalloprotease and its isoforms in CNS and tes
A:Reference number: JC7265
A:Contents: Brain and testis
A:Accession: JC7265
A:Molecule type: mRNA
A:Residues: 1-774 <TAN>
C:Genetics:
A:Gene: nepII
C:Superfamily: neprilysin
C:Keywords: brain; glycoprotein; hydrolase; metalloproteinase; neuropeptide; testis; tra

Query Match 4.2%; Score 94; DB 2; Length 774;
Best Local Similarity 21.3%; Pred. No. 15;
Matches 82; Conservative 44; Mismatches 123; Indels 136; Gaps 18;

Qy 39 SEPRDTQLSQDLGGTAMDLPNRTVRVEDNHSYVSRLYGSPSPHSRELVDVAEAN 98
      ||| : : : : : : : : : : : : : : : : : : : : : : : :
Db 182 SEPLLNVLDL-IGGWPVAMDKW--NET-----MGPKWELERQLAVLNSQFN 224
      ||| : : : : : : : : : : : : : : : : : : : : : : : :

Qy 99 RSQVKIHTLSNTHRQASRVLSFDPPFYGHPLRQITATGGTIFMGDVHRLMTA----- 154
      ||| : : : : : : : : : : : : : : : : : : : : : : : :
Db 225 R-RVLIDLFIWDDQNSRRHYIIDQPTLGMPSRE-----YFKEK-SHRVREAYLQF 275
      ||| : : : : : : : : : : : : : : : : : : : : : : : :

Qy 155 -TQYVAPLMAFN-PGYSDNSTVTVYFNGTVFVQWDHVLQGWEDKGSFTFQAALHHDG 212
      ||| : : : : : : : : : : : : : : : : : : : : : : : :
Db 276 MTSVATMLRDLNLPGETD-----LVQ----- 297

Qy 213 RIVPAYKEIPMSVPEISSQHPVKIGLSDAFMIPLNPSDPVPESRRRIFE-YHRIELDP- 270
      ||| : : : : : : : : : : : : : : : : : : : : : : : :
Db 298 -----SEMAQVLH-LETHLANA-----TVPEKRRHDVTALYHRMGLEEL 335
      ||| : : : : : : : : : : : : : : : : : : : : : : : :

Qy 271 -----SKVTSNAVEFTPLPTCLOH-----RSCDACMSSDLTFNCS 306
      ||| : : : : : : : : : : : : : : : : : : : : : : : :
Db 336 QERFGLGFNWTLPFQNVLSVQVELLPNEEVVYIGIPYLENLEEIIDVFPQTLQNVLV 395

Qy 307 WCHVLQRCSSGFDRYQEWMDYGCA-----QEAEGRMCEDFQDEHDHSA----- 350
      ||| : : : : : : : : : : : : : : : : : : : : : : : :
Db 396 WRLVLDRIGLSLSQRFKEARVDYRKALYGTMTMEEVWRRECYSVYNNMESAVGSLYIKRAF 455
      ||| : : : : : : : : : : : : : : : : : : : : : : : :

Qy 351 SPDTFSFYDGLDTTSSSLFIDSL 375
      ||| : : : : : : : : : : : : : : : : : : : : : : : :
Db 456 SKDS--KSIVSELIEKIRSVFVDNL 478
      ||| : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 14
S70642
ubiquitin ligase Nedda4 - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S70642
R:Staub, O.; Dho, S.; Henry, P.C.; Correa, J.; Ishikawa, T.; McGlade, J.; Rotin, D.
EMBO J. 15, 2371-2380, 1996
A>Title: WW domains of Nedda4 bind to the proline-rich PY motifs in the epithelial Na(+)
A:Reference number: S70642; MUID:96221297; PMID:8665844
A:Accession: S70642
A>Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-887 <STA>
A:Cross-references: UNIPROT:Q62940; EMBL:U50842; NID:g1293646; PIDN:AAB48949.1; PID:g129
C:Genetics:
```

```
A:Gene: Nedda4
C:Superfamily: rat ubiquitin-protein ligase; protein kinase C C2 region homology; ubiqui
F;54-167/Domain: protein kinase C C2 region homology <KC2>
F;246-283/Domain: WW repeat homology <WW1>
F;402-439/Domain: WW repeat homology <WW2>
F;459-496/Domain: WW repeat homology <WW3>
F;555-881/Domain: ubiquitin-protein ligase homology <UBI>

Query Match 4.2%; Score 93.5; DB 2; Length 887;
Best Local Similarity 19.1%; Pred. No. 20;
Matches 90; Conservative 54; Mismatches 151; Indels 175; Gaps 24;

Qy 5 QPQAGAG-----HDEGPG-----SCWAAKGTVRG-----WNRRARES----- 34
      ||| : : : : : : : : : : : : : : : : : : : : : : : :
Db 232 QPDAATHLQHPPEPSPPLPGWEERQDVLGRYYVNHESRTQWKPKPEDDLTDENGDI 291
      ||| : : : : : : : : : : : : : : : : : : : : : : : :

Qy 35 --PGHVSEPDRTQLSQDLGGTAMDLPNRTT-----VVEDNHSYVSR-LYGPSEP 85
      ||| : : : : : : : : : : : : : : : : : : : : : : : :
Db 292 QLQAHGAFTRRQISEVDVG-----PDNHESPENWEIVREDENTYISGQAVQSPPSG 343
      ||| : : : : : : : : : : : : : : : : : : : : : : : :

Qy 86 HSRELWVDVAEANRSQVKIHTLSNTHRQASRVLSFDPPFYGHPLRQITATGGTIFPMG 145
      ||| : : : : : : : : : : : : : : : : : : : : : : : :
Db 344 HP-DVQVRLAE-----ELDTRLT-----MYGNPATSQPVTSNHSRSG 380
      ||| : : : : : : : : : : : : : : : : : : : : : : : :

Qy 146 DVIHRLMTATQYVAPLM-----ANFNPGY-----SDNSTVYFDNGTVFVQWDHVLQ--- 194
      ||| : : : : : : : : : : : : : : : : : : : : : : : :
Db 381 GSSQTCIFEEQPTLPVLLPTSSGLPGWEEKQDGRGSIYVDHNSK-TTWSKFTMQDDP 439
      ||| : : : : : : : : : : : : : : : : : : : : : : : :

Qy 195 -----GWEDKGSFTFQAALHHDGRIVFAYKAIPIMSVPEISS 230
      ||| : : : : : : : : : : : : : : : : : : : : : : : :
Db 440 RSKIPAHLRGKTPVDSNDLGLPFGWEER-----THTDGRVFFINHNIKKTQWEDPR 491
      ||| : : : : : : : : : : : : : : : : : : : : : : : :

Qy 231 SQHPVKTGLSDAFMIPLNPSDPVESR-RRSIFEVHRIELDPSSKVTSMASAVEFTPLPTCLO 289
      ||| : : : : : : : : : : : : : : : : : : : : : : : :
Db 492 MQNVAITG-----PAEPYSRDYKRYKFFRRKKLKKQ-----TDIPNKF 530
      ||| : : : : : : : : : : : : : : : : : : : : : : : :

Qy 290 HRSDCACMSSDLTFNCSGWCHVLRQCSGFDRYQEWMDYGCAQEAEGRMCEDFQDE---D 346
      ||| : : : : : : : : : : : : : : : : : : : : : : : :
Db 531 MK-----LRRANILEDYSRR-INGVKRADFLKARLWIEFGEGKGLD 570
      ||| : : : : : : : : : : : : : : : : : : : : : : : :

Qy 347 HDASASP-----TSFSFYDGLDTTSSSLFIDSLTTEDDT-KLNYPAG 388
      ||| : : : : : : : : : : : : : : : : : : : : : : : :
Db 571 YGGVAREWFLLISKEMFNYYG-----LFEYSATDNYTLQINPSG 612
      ||| : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 15
JC2349
protein-tyrosine-phosphatase (SC 3.1.3.48), receptor type N precursor - mouse
N:Alternate names: protein-tyrosine-phosphatase IA-2
C:Species: Mus musculus (house mouse)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: JC2349; S40291; I48721
R:Lu, J.; Notkins, A.L.; Lan, M.S.
Biochem. Biophys. Res. Commun. 204, 930-936, 1994
A>Title: Isolation, sequence and expression of a novel mouse brain cDNA, mIA-2, and its
A:Reference number: JC2349; MUID:95071416; PMID:7980563
A:Accession: JC2349
A:Molecule type: mRNA
A:Residues: 1-979 <LUJ>
A:Cross-references: UNIPROT:Q60673; EMBL:U11812; NID:G563737; PIDN:AAA52102.1; PID:G5637
A:Experimental source: brain
R:Hendriks, W.; Brugman, C.; Zeeuwen, P.; Schepens, J.; Wieringa, B.
submitted to the EMBL Data Library, June 1993
A:Description: Assessment of the expression levels of murine protein-tyrosine phosphatase
A:Reference number: S40291
A:Accession: S40291
A:Molecule type: mRNA
A:Residues: 801-837, 839-852, 'T', 854-907 <HEN>
A:Cross-references: EMBL:Z23060; NID:g438157; PIDN:CAA80595.1; PID:g438158
R:Magistrulli, G.; Covinin, N.; Mosca, M.; Lippoli, G.; Isacchi, A.
Biochem. Biophys. Res. Commun. 217, 154-161, 1995
A>Title: Expression of PTP35, the murine homologue of the PTP2 se-related sequences 1A-2
A:Reference number: I48721; MUID:96095652; PMID:8526904
```



A;Accession: I48721  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 'MFPCARGSESPGR', 1-165, 'GDGAGA', 170-362, 'L', 364-614, 'V', 616-674, 'T', 676-858  
A;Cross-references: EMBL:X74438; NID:g1089901; PIDN:CAA52453.1; PID:g1089902  
C;Superfamily: protein-tyrosine-phosphatase, receptor type N; protein-tyrosine-phosphatase  
C;Keywords: brain; glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane  
F;1-37/Domain: signal sequence #status predicted <SIG>  
F;38-979/Product: protein-tyrosine-phosphatase, receptor type N #status predicted <MAT>  
F;38-979/Domain: extracellular #status predicted <EXT>  
F;577-598/Domain: transmembrane #status predicted <TM>  
F;696-979/Domain: intracellular #status predicted <INT>  
F;734-958/Domain: protein-tyrosine-phosphatase homology <PTP2>  
F;506,524/Binding site: carboxylate (Asn) (covalent) #status predicted  
F;909/Active site: Cys (phosphocysteine intermediate) #status predicted  
F;915/Binding site: substrate phosphate (Arg) #status predicted

Query Match 4.2%; Score 93.5; DB 1; Length 979;  
Best Local Similarity 23.0%; Pred. No. 23;  
Matches 38; Conservative 23; Mismatches 55; Indels 49; Gaps 7;

Qy	258	RSIFEHRIELDPKSVTSMGAVEPTPLTCLQHRSCDACMSSDLTFNC--SWC-----	308
Db	639	KSLFNRAEGQPEPRVSVSG-QFS-----DAAQASPSHSSSWCEEPAAQAN	686
Qy	309	-----HVLQRCSGFDYRQFWMYDYGCAQAEGRMCBDFQDEHDSDASPD	353
Db	687	MDISTGHMILAYMEDHLNR-----DLAKWQAL-CAYQAEPTCAAQDESNIKKNRH	740
Qy	354	TSFSPYDG-----DLTTSSSLFIDSLTETDTKLNPYAGGDG	391
Db	741	PDFLPYDHARIKLVKVESPSRSDYINASPIEHDPRMPAYIATQG	785

Search completed: January 28, 2005, 22:12:44  
Job time : 30.3934 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 28, 2005, 21:55:21 ; Search time 139.695 Seconds  
(without alignments)  
1688.701 Million cell updates/sec

Title: US-09-918-715-230\_COPY\_18\_427

Perfect score: 2218

Sequence: 1 ALSPPQAGHDEGPGSGWAA.....GLQNNLSPKTKGTFVHLGTI 410

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt\_02.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2218	100.0	500	2	Q9HCT9
2	2215	99.9	500	2	Q8IUK5
3	1799.5	81.1	500	2	Q91ZV7
4	1793.5	80.9	500	2	Q9CWV5
5	1780	80.3	507	2	Q8BM20
6	1326	59.8	351	2	Q6ZSC8
7	1326	59.8	351	2	BAC87025
8	1066.5	48.1	529	2	Q6UX71
9	1066.5	48.1	529	2	Q96PD9
10	1066.5	48.1	529	2	AAQ88850
11	1044	47.1	530	2	Q6PEY5
12	1044	47.1	530	2	Q9DC11
13	1044	47.1	530	2	Q91ZV6
14	1044	47.1	530	2	AAH57881
15	1034.5	46.6	513	2	Q6DE92
16	900	40.6	480	2	Q96E59
17	624.5	28.2	625	2	Q9W2V9
18	602	27.1	498	2	Q18500
19	308	13.9	274	2	Q7PJF6
20	274.5	12.4	384	2	Q7Q2J8
21	253	11.4	77	2	Q7PJF7
22	159.5	7.2	343	2	Q6PYV2
23	159.5	7.2	343	2	AA568255
24	131	5.9	190	2	Q86E23
25	126	5.7	1161	2	Q94901
26	121.5	5.5	2119	2	Q8CJH3
27	117	5.3	308	2	Q9UN94
28	115.5	5.2	1568	2	Q60486
29	114	5.1	1324	2	Q7YZ28
30	111.5	5.0	366	2	Q9UN95
31	111.5	5.0	877	2	Q9H3Q6

32	111.5	5.0	878	2	Q9H3Q7
33	111.5	5.0	1217	2	Q9UKW9
34	107	4.8	537	1	PPCK_RHISN
35	106.5	4.8	315	2	Q6URR8
36	106.5	4.8	315	2	AAQ62573
37	106.5	4.8	901	2	Q9H195
38	105.5	4.8	878	2	Q9GZ22
39	105	4.7	582	2	Q6PB14
40	105	4.7	582	2	AAH59696
41	104.5	4.7	276	2	Q9FIT3
42	104.5	4.7	514	2	Q9FB48
43	103.5	4.7	282	2	Q6PVV3
44	103.5	4.7	282	2	AA568254
45	102	4.6	342	2	O68868

ALIGNMENTS

RESULT 1  
Q9HCT9 ID Q9HCT9 PRELIMINARY; PRT; 500 AA.  
AC Q9HCT9;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Tumor endothelial marker 7 precursor (tumor endothelial marker 3 precursor).  
DE precursor.  
GN Name=TEM7;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20407466; PubMed=10947988;  
RA St Croix B., Rago C., Velculescu V., Traverso G., Romans K.E., Montgomery E., Lal A., Riggins G.J., Lengauer C., Vogelstein B., Kinzler K.W.;  
RA "Genes expressed in human tumor endothelium."  
RL Science 289:1197-1202(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA St Croix B., Vogelstein B., Kinzler K.W.;  
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21443268; PubMed=11559528;  
RA Carson-Walter E.B., Watkins D.N., Nanda A., Vogelstein B., Kinzler K.W., St Croix B.;  
RL "Cell surface tumor endothelial markers are conserved in mice and humans."  
RL Cancer Res. 61:6649-6655(2001).  
DR EMBL; AF279144; AAC00869.2; -.  
DR EMBL; AF378753; AAL11990.1; -.  
DR GO; GO:0001525; P:angiogenesis; NAS.  
DR InterPro; IPR001659; Plexin-like.  
DR InterPro; IPR002165; Plexin\_repeat.  
DR Pfam; PF01437; PSI; 1.  
DR SMART; SMO0423; PSI; 1.  
DR Signal.  
KW SIGNAL  
FT CHAIN  
FT SIGNAL  
SQ SEQUENCE 500 AA; 55760 MW; C545A16619EEDBED CRC64;

Query Match 100.0%; Score 2218; DB 2; Length 500;  
Best Local Similarity 100.0%; Pred. No. 4.2e-174;  
Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ALSPPQAGHDEGPGSGWAAKGTVRGRRRARESPGHVSEPDRTQLSQDLGGGTLAMDTL	60
Db	18	ALSPPQAGHDEGPGSGWAAKGTVRGRRRARESPGHVSEPDRTQLSQDLGGGTLAMDTL	77

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Qy 61 PDNRTRVEDNHSYVSRLYGSPHSGHRELWVDVAENRSQVKIHTILSNTHRQASRVVL 120
Db 78 PDNRTRVEDNHSYVSRLYGSPHSGHRELWVDVAENRSQVKIHTILSNTHRQASRVVL 137
Qy 121 SFDPFFYGHPLRQITITATGGFIFMGDVIHRMLTATQVAPLMANFNPGYSDNSTVVYFDN 180
Db 138 SFDPFFYGHPLRQITITATGGFIFMGDVIHRMLTATQVAPLMANFNPGYSDNSTVVYFDN 197
Qy 181 GTVFVQWDHVYLGQWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHPVKTGLS 240
Db 198 GTVFVQWDHVYLGQWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHPVKTGLS 257
Qy 241 DAFMILNPSDPVPSRRRSIFPEYHRIELDPKVTSMGSAVEFTPLPTCLQHRSCDACMSSD 300
Db 258 DAFMILNPSDPVPSRRRSIFPEYHRIELDPKVTSMGSAVEFTPLPTCLQHRSCDACMSSD 317
Qy 301 LTFNCSCHVLRQCSGFDYRQEWMDYGCQAEGRMCEDFQDEHDSASPDTSFSPYD 360
Db 318 LTFNCSCHVLRQCSGFDYRQEWMDYGCQAEGRMCEDFQDEHDSASPDTSFSPYD 377
Qy 361 GDLTTSSSLFIDSLLTTEDDTKLNYPAGGDLQNNLSPKTKGTPVHLGTI 410
Db 378 GDLTTSSSLFIDSLLTTEDDTKLNYPAGGDLQNNLSPKTKGTPVHLGTI 427

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## RESULT 2

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Q81UKS PRELIMINARY; PRT; 500 AA.
AC Q81UKS;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Plexin domain containing 1,.
GN Name=PLXDC1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinstead J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis"
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC036059; AAH36059.1; -.
DR Genew; HGNC:20945; PLXDC1.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007275; P:development; IEA.
DR InterPro; IPR003659; Plexin-like.

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DR InterPro; IPR002165; Plexin_repeat.
DR Pfam; PF01437; PSI; 1.
DR SMART; SM00423; PSI; 1.
SQ SEQUENCE 500 AA; 55778 MW; 3FA4P9D98A514ABF CRC64;

Query Match 99.9%; Score 2215; DB 2; Length 500;
Best Local Similarity 99.8%; Pred. No. 7.5e-174;
Matches 409; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALSPPQAGHDEGPGSGAAAKGTVRGWNRRAARESPGHVSEPDRTQLSQDLGGGTLAMDTL 60
Db 18 ALSPPQAGHDEGPGSGAAAKGTVRGWNRRAARESPGHVSEPDRTQLSQDLGGGTLAMDTL 77
Qy 61 PDNRTRVEDNHSYVSRLYGSPHSGHRELWVDVAENRSQVKIHTILSNTHRQASRVVL 120
Db 78 PDNRTRVEDNHSYVSRLYGSPHSGHRELWVDVAENRSQVKIHTILSNTHRQASRVVL 137
Qy 121 SFDPFFYGHPLRQITITATGGFIFMGDVIHRMLTATQVAPLMANFNPGYSDNSTVVYFDN 180
Db 138 SFDPFFYGHPLRQITITATGGFIFMGDVIHRMLTATQVAPLMANFNPGYSDNSTVVYFDN 197
Qy 181 GTVFVQWDHVYLGQWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHPVKTGLS 240
Db 198 GTVFVQWDHVYLGQWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHPVKTGLS 257
Qy 241 DAFMILNPSDPVPSRRRSIFPEYHRIELDPKVTSMGSAVEFTPLPTCLQHRSCDACMSSD 300
Db 258 DAFMILNPSDPVPSRRRSIFPEYHRIELDPKVTSMGSAVEFTPLPTCLQHRSCDACMSSD 317
Qy 301 LTFNCSCHVLRQCSGFDYRQEWMDYGCQAEGRMCEDFQDEHDSASPDTSFSPYD 360
Db 318 LTFNCSCHVLRQCSGFDYRQEWMDYGCQAEGRMCEDFQDEHDSASPDTSFSPYD 377
Qy 361 GDLTTSSSLFIDSLLTTEDDTKLNYPAGGDLQNNLSPKTKGTPVHLGTI 410
Db 378 GDLTTSSSLFIDSLLTTEDDTKLNYPAGGDLQNNLSPKTKGTPVHLGTI 427

RESULT 3
Q91ZV7 PRELIMINARY; PRT; 500 AA.
AC Q91ZV7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Tumor endothelial marker 7 precursor.
GN Name=Plxcl1; Synonyms=Tem7;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21443268; PubMed=11559528;
RA Carson-Walter E.B., Watkins D.N., Nanda A., Vogelstein B.,
RA Kinzler K.W., St Croix B.;
RT "Cell surface tumor endothelial markers are conserved in mice and
RT humans.";
RL Cancer Res. 61:6649-6655 (2001).
DR EMBL; AF378760; AAL11997.1; -.
DR MGD; MGI:1919574; Plxcl1.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007275; P:development; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003659; plexin-like.
DR InterPro; IPR002165; plexin_repeat.
DR Pfam; PF01437; PSI; 1.
DR SMART; SM00423; PSI; 1.
DR Signal.
KW SIGNAL.
FT CHAIN 1 19 Potential.
FT CHAIN 20 500 tumor endothelial marker 7.
SQ SEQUENCE 500 AA; 55693 MW; 14FE25512A319DAF CRC64;

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```
Query Match      81.1%; Score 1799.5; DB 2; Length 500;
Best Local Similarity 80.7%; Pred. No. 1.3e-139;
Matches 331; Conservative 39; Mismatches 39; Indels 1; Gaps 1;

Qy 1 ALSPPQAGHDEGPGSCWAAKGTVRGNRRARESPGHVSEPDRTQLSQDLGGGTAMDTL 60
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
19 ALSPATPAGHNEGQDSAWTAKTRQGSRRRPRESPAQVLKPGKTQLSQDLGGGSLAIDTL 78
Qy 61 PDNTRVVEDNHSYVYVSRLYGSPSPHRELWVDVAEANSRQVKTHTILSNTHRSQSRVVL 120
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
79 PDNTRVVEDNHNHYVSRVYVGPGEKQSDLVAVANRSHVKHRIILSSSHRQASRVVL 138
Qy 121 SFDPFFYGHPLRQITTIATGGFIFMGDVTHRMILTATQYVAPLMANFNPGYSNVTVPFDN 180
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
139 SFDPFFYGHPLRQITTIATGGFIFMGDLHRLMILTATQYVAPLMANFNPGYSNVTVPFDN 198
Qy 181 GTVFVQWDHVYLVQWEDKGSFTFOAALHHDGRIVFAYKEIPMVSPEISSQHPVKTGLS 240
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
199 GTVFVQWDHVYLVQWEDRGSFTFOAALHHDGRIVFAYKEIPMAVLDISSAQHPVKAGLS 258
Qy 241 DAFMLNPSDPVPSRRRSIFEVHRIELDPSSKVTSMASAVEFTPLPTCLQHSRCDACWSSD 300
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
259 DAFMLNPSPEVPSQRTIFEXHVELDSSKITTSVAVEFTPLPTCLQHSRCDTCVSSN 318
Qy 301 LTFNCSWCHVLQRCSSGFDRIYRQEWMDYGCQAEGRMCEDFQDEHDSASPTDSFSPYD 360
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
319 LTFNCSWCHVLQRCSSGFDRIYRQEWLTYGCQAEGKTCEDFQDDSHYSASPDSSFSFPN 378
Qy 361 GDLTTSSSLFIDSLTTEDDTKLPYAGGDLGNLSPKTKGTPVHLGTI 410
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
379 GD-STTSSSLFIDSLTTEDDTKLPYAGGDLGNLSPKTKGTPVHLGTI 427

RESULT 4
Q9CWV5 PRELIMINARY; PRT; 500 AA.
AC Q9CWV5;
AT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE Mus musculus ES cells cDNA, RIKEN full-length enriched library,
clone:241003107 product:TUMOR ENDOTHELIAL MARKER 7 homolog.
GN Name=Plx1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=927253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
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RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Komoto H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Inotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito K., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK010361; BAB26881.1; -.
DR MGD; MGI:1919574; Plx1cd1.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007275; P:development; IEA.
DR InterPro; IPR007110; Ig-like
DR InterPro; IPR003659; Plexin-like.
DR InterPro; IPR002165; Plexin_repeat.
DR Pfam; PF01437; PSI; 1.
DR SMART; SM00423; PSI; 1.
SQ SEQUENCE 500 AA; 55635 MW; 802D6865F8CA18BD CRC64;

Query Match      80.9%; Score 1793.5; DB 2; Length 500;
Best Local Similarity 80.5%; Pred. No. 4.2e-139;
Matches 330; Conservative 39; Mismatches 40; Indels 1; Gaps 1;

Qy 1 ALSPPQAGHDEGPGSCWAAKGTVRGNRRARESPGHVSEPDRTQLSQDLGGGTAMDTL 60
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
19 ALSPATPAGHNEGQDSAWTAKTRQGSRRRPRESPAQVLKPGKTQLSQDLGGGSLAIDTL 78
Qy 61 PDNTRVVEDNHSYVYVSRLYGSPSPHRELWVDVAEANSRQVKTHTILSNTHRSQSRVVL 120
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
79 PDNTRVVEDNHNHYVSRVYVGPGEKQSDLVAVANRSHVKHRIILSSSHRQASRVVL 138
Qy 121 SFDPFFYGHPLRQITTIATGGFIFMGDVTHRMILTATQYVAPLMANFNPGYSNVTVPFDN 180
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
139 SFDPFFYGHPLRQITTIATGGFIFMGDLHRLMILTATQYVAPLMANFNPGYSNVTVPFDN 198
Qy 181 GTVFVQWDHVYLVQWEDKGSFTFOAALHHDGRIVFAYKEIPMVSPEISSQHPVKTGLS 240
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
199 GTVFVQWDHVYLVQWEDRGSFTFOAALHHDGRIVFAYKEIPMAVLDISSAQHPVKAGLS 258
Qy 241 DAFMLNPSDPVPSRRRSIFEVHRIELDPSSKVTSMASAVEFTPLPTCLQHSRCDACWSSD 300
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
259 DAFMLNPSPEVPSQRTIFEXHVELDSSKITTSVAVEFTPLPTCLQHSRCDTCVSSN 318
Qy 301 LTFNCSWCHVLQRCSSGFDRIYRQEWMDYGCQAEGRMCEDFQDEHDSASPTDSFSPYD 360
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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319 LTFNCWCHVQLRCSSGFDYRQEWLTYGCAQAEAGKTCEDFQDDSHYSASPDSSFPFN 378
361 GDLTTSSSLFIDSLTTEDDTKLNYPYAGGDLQNNLSPKTKGTPVHLGTI 410
379 GD-STTSSSLFIDSLTTEDDTKLNYPYAGGDLQNNLSPKTKGTPVHLGTI 427

RESULT 5
Q8BM20 PRELIMINARY; PRT; 507 AA.
AC Q8BM20;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 16 days neonate cerebellum cDNA, RIKEN full-length
DE enriched library, clone:9630040L07 product:TUMOR ENDOTHELIAL MARKER 7
DE homolog.
GN Name=Plx1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 403:685-690(2001).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
[4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayateu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
[5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=20530913; PubMed=11078861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsuoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Okawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
[6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayateu N., Hiramoto K., Hiraoka T., Hirozane T.,

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RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akai S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK036144; BAC29318.1; -.
DR MGD; MGI:1919574; Plx1.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004872; P:receptor activity; IEA.
DR GO; GO:0007275; P:development; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003659; plexin-like.
DR InterPro; IPR002165; plexin_repeat.
DR Pfam; PF01437; PSI; 1.
DR SMART; SM00423; PSI; 1.
SQ SEQUENCE 507 AA; 56332 MW; C2D50B44561C3415 CRC64;

Query Match 80.3%; Score 1780; DB 2; Length 507;
Best Local Similarity 79.1%; Pred. No. 5.5e-138;
Matches 330; Conservative 39; Mismatches 40; Indels 8; Gaps 2;

Qy 1 ALSPPGAGHDEGPGCGAAKGTVRGWRARSPGHVSBDRTQSLDGGGTAMDITL 60
Db 19 ALSPPATPAGHNEGQDSAWTAKTRQGSRRPRSPQAVLPKPKTQSLDGGGSLADITL 78
Qy 61 PDNRTRVV-----EDNHYVSRLYSGPSEPHSRRLWVDVAENRSQVKIHTILSNTHR 113
Db 79 PDNRTRVVALSLSPQEDNHNHYVSRVYVPGKQSDLVAVANRSHVKIHLSSSHR 138
Qy 114 QARVVLSPDPFPYGHPLRQITATGGFIFMGDVIHMLTATQVAPLPMANFPGYDNS 173
Db 139 QASRVVLSFDPFPYGHPLRQITATGGFIFMGDMLHMLTATQVAPLPMANFPGYDNS 198
Qy 174 TVVYFDNGTVVQWDHVLQGWEDKGSFTFOALHHDGRIVFAYKEIPMSVPEISSQH 233
Db 199 TVAYFDNGTVVQWDHVLQDREDRGSFTFOALHHDGRIVFAYKEIPMAVLDISSAQH 258
Qy 234 PVKTGLSDAFMILNPSDPVPESSRRSIFHYHRIELDPKVTSMASAVEFTPLPTCLQHRSC 293
Db 259 PVKAGLSDAFMILNPSDEVASQRTTFEYHVRVELDSKITTSAVEFTPLPTCLQHQSC 318
Qy 294 DACMSSDLTFCNSCHVQLRCSSGFDYRQEWLTYGCAQAEAGKTCEDFQDDSHYSASP 353
Db 319 DTCVSSNLTFNCWCHVQLRCSSGFDYRQEWLTYGCAQAEAGKTCEDFQDDSHYSASP 378
Qy 354 TSFSPYDGLTTTSSSLFIDSLTTEDDTKLNYPYAGGDLQNNLSPKTKGTPVHLGTI 410
Db 379 SSFSPFNGD-STTSSSLFIDSLTTEDDTKLNYPYAGGDLQNNLSPKTKGTPVHLGTI 434

RESULT 6
Q6ZSC8 PRELIMINARY; PRT; 351 AA.
ID Q6ZSC8
AC Q6ZSC8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein FLJ45632.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Oshima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K.,
RA Arita M., Mueashino K., Youki H., Hara H., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Umezawa A., Imabayashi H.,
RA Fukuma M., Hata J., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y.,
RA Saito K., Nishikawa T., Kimura K., Yamashita H., Matsuo K.,

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Qy 234 PVKTGLSDAFVWVHRIQIIPNRRRTIYEHVRLQMSKIINISAVEMTPLPTCLQHRSC 293
Db 275 PVKGLSDAFVWVHRIQIIPNRRRTIYEHVRLQMSKIINISAVEMTPLPTCLQHRNC 334

Qy 294 DACMSSDLTFCNSCHVLQRCSSGDFRYRQEMWMDYGCABEGRMCDFQDEHDSASPD 353
Db 335 GPCVSSQIGFNCSCWCKLQRCSSGDFRHRQDWDVSGCPESKEKMCENTEPVTSRRTT 394

Qy 354 T--SFSYDGLTWTTS---SSLFIDSLLTDDTKLNPYAGDGLQ--NNLSPKTKGTPVHL 407
Db 395 TVGATTQFRVLTTTTRRAVTSQPTSLPTEDDTKIALHLKDNKGASTDSDAAEKKGGTLHA 454

Qy 408 GTI 410
Db 455 GLI 457

RESULT 9
Q96PD9 PRELIMINARY; PRT; 529 AA.
ID Q96PD9 PRELIMINARY; PRT; 529 AA.
AC Q96PD9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Tumor endothelial marker 7-related precursor.
GN Name="TEM7R";
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21443268; PubMed=11559528;
RA Carson-Walter E.B., Watkins D.N., Nanda A., Vogelstein B.,
RA Kinzler K.W., St Croix B.;
RT "Cell surface tumor endothelial markers are conserved in mice and
RT humans.";
RL Cancer Res. 61:6649-6655 (2001).
DR EMBL; AF378757; AAL1194.1; -.
DR Genew; HGNC:21013; PLXDC2.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004872; P:receptor activity; IEA.
DR GO; GO:0007275; P:development; IEA.
DR InterPro; IPR003659; Plexin-like.
DR InterPro; IPR002165; Plexin_repeat.
DR Pfam; PF01437; PSI; 1.
DR SMART; SM00423; PSI; 1.
KW Signal.
FT SIGNAL
FT CHAIN
SQ SEQUENCE 529 AA; 59583 MW; D44A0975DF894840 CRC64;

Query Match 48.1%; Score 1066.5; DB 2; Length 529;
Best Local Similarity 56.5%; Pred. No. 3.8e-79;
Matches 205; Conservative 63; Mismatches 88; Indels 7; Gaps 4;

Qy 55 LAMDTLPDNRTRVVED-NHSYVSRLYGSPSPHRELWVDVAENRSQVKIHTLSNTHR 113
Db 95 LLLDDGQDNNTQIEEDTDHNYISRIYGPSDSASRDLWVNIDQMKDKVKIHGILSNTHR 154

Qy 114 QASRVVLSFDPFPGHPLRQITATGGFIFMGDVIHRLMTATQYVAPLMAFNPNPGYSDNS 173
Db 155 QAARVNLSPDFPFGHFLREITVATGGFIYGEVHRLMTATQYIAPLMAFNDFPSVRNS 214

Qy 174 TVVYFDNGTVFVQWQDHYVQLQWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPEISSQH 233
Db 215 TVRYFDNGTALVQWQDHYVQLQWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPEISSQH 274

Qy 234 PVKTGLSDAFVWVHRIQIIPNRRRTIYEHVRLQMSKIINISAVEMTPLPTCLQHRSC 293
Db 275 PVKGLSDAFVWVHRIQIIPNRRRTIYEHVRLQMSKIINISAVEMTPLPTCLQHRNC 334

Qy 294 DACMSSDLTFCNSCHVLQRCSSGDFRYRQEMWMDYGCABEGRMCDFQDEHDSASPD 353
Db 335 GPCVSSQIGFNCSCWCKLQRCSSGDFRHRQDWDVSGCPESKEKMCENTEPVTSRRTT 394

Qy 354 T--SFSYDGLTWTTS---SSLFIDSLLTDDTKLNPYAGDGLQ--NNLSPKTKGTPVHL 407
Db 395 TVGATTQFRVLTTTTRRAVTSQPTSLPTEDDTKIALHLKDNKGASTDSDAAEKKGGTLHA 454

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Qy 294 DACMSSDLTFCNSCHVLQRCSSGDFRYRQEMWMDYGCABEGRMCDFQDEHDSASPD 353
Db 335 GPCVSSQIGFNCSCWCKLQRCSSGDFRHRQDWDVSGCPESKEKMCENTEPVTSRRTT 394

Qy 354 T--SFSYDGLTWTTS---SSLFIDSLLTDDTKLNPYAGDGLQ--NNLSPKTKGTPVHL 407
Db 395 TVGATTQFRVLTTTTRRAVTSQPTSLPTEDDTKIALHLKDNKGASTDSDAAEKKGGTLHA 454

Qy 408 GTI 410
Db 455 GLI 457

RESULT 10
AAQ88850 PRELIMINARY; PRT; 529 AA.
AC AAQ88850;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE ARP2514.
GN UNQ2514.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12975309;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liaw D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seehagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
RT Effort to Identify Novel Human Secreted and Transmembrane Proteins: A
RT Bioinformatics Assessment.";
RL Genome Res. 13:2265-2270 (2003).
DR EMBL; AY358486; AAQ88850.1; -.
SQ SEQUENCE 529 AA; 59583 MW; CCE911D6DF837B40 CRC64;

Query Match 48.1%; Score 1066.5; DB 2; Length 529;
Best Local Similarity 56.5%; Pred. No. 3.8e-79;
Matches 205; Conservative 63; Mismatches 88; Indels 7; Gaps 4;

Qy 55 LAMDTLPDNRTRVVED-NHSYVSRLYGSPSPHRELWVDVAENRSQVKIHTLSNTHR 113
Db 95 LLLDDGQDNNTQIEEDTDHNYISRIYGPSDSASRDLWVNIDQMKDKVKIHGILSNTHR 154

Qy 114 QASRVVLSFDPFPGHPLRQITATGGFIFMGDVIHRLMTATQYVAPLMAFNPNPGYSDNS 173
Db 155 QAARVNLSPDFPFGHFLREITVATGGFIYGEVHRLMTATQYIAPLMAFNDFPSVRNS 214

Qy 174 TVVYFDNGTVFVQWQDHYVQLQWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPEISSQH 233
Db 215 TVRYFDNGTALVQWQDHYVQLQWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPEISSQH 274

Qy 234 PVKTGLSDAFVWVHRIQIIPNRRRTIYEHVRLQMSKIINISAVEMTPLPTCLQHRSC 293
Db 275 PVKGLSDAFVWVHRIQIIPNRRRTIYEHVRLQMSKIINISAVEMTPLPTCLQHRNC 334

Qy 294 DACMSSDLTFCNSCHVLQRCSSGDFRYRQEMWMDYGCABEGRMCDFQDEHDSASPD 353
Db 335 GPCVSSQIGFNCSCWCKLQRCSSGDFRHRQDWDVSGCPESKEKMCENTEPVTSRRTT 394

Qy 354 T--SFSYDGLTWTTS---SSLFIDSLLTDDTKLNPYAGDGLQ--NNLSPKTKGTPVHL 407
Db 395 TVGATTQFRVLTTTTRRAVTSQPTSLPTEDDTKIALHLKDNKGASTDSDAAEKKGGTLHA 454

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QY 408 GTI 410
DB 455 GII 457

RESULT 11
Q6PETS PRELIMINARY; PRT; 530 AA.
AC Q6PETS;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Tumor endothelial marker 7-related.
GN Name=Plxdc2;
OS Mus musculus (Mouse).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NMRI; TISSUE=Mammary tumor. WAP-Tag model. 5 months old;
RX MEDLINE=22389257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
EL proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NMRI; TISSUE=Mammary tumor. WAP-Tag model. 5 months old;
RA Strausberg R.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC057881; AAH57881.1;
DR InterPro; IPR003659; Plexin-like.
DR Pfam; PF01437; PSI; 1.
DR SMART; SM00423; PSI; 1.
SQ SEQUENCE 530 AA; 59646 MW; D7256C02073417FC CRC64;

Query Match 47.1%; Score 1044; DB 2; Length 530;
Best Local Similarity 51.3%; Pred. No. 2.7e-77;
Matches 203; Conservative 67; Mismatches 112; Indels 14; Gaps 6;

QY 27 WNRARSPGHVSPDRQLSQ----DLGGTGLANDTLPLDNRTRVED-NHSYVYSLRG 81
DB 65 WKRNV--DPFKAVDTNRASMGQASPEKGFDTLLDDGQNNNTQLEEDTDHNYISRYG 122

QY 82 PSEPHSRLVDVAEANSQVKIHTILSNTHRQASRVVLSDFPFYGHPLRQITATCGF 141
DB 123 PADASRDLVNIDQMEKDKVKIHGILSNTHRQARVNLSDFFPYGHFLNEVITATGGF 182

QY 142 IFMGDVIHRLMTATQYVAPLMANFPGVSDNSTVYFDFNGTVFVQMDHVLQGWEDKGS 201
DB 183 IYTGVEVHRLMTATQYIAPLMANFDPSPVSRNSTVRYFDFNGTALVQMDHVLQDNYNLGS 242

QY 202 FTFOALHHDCRIYFAYKEIPMSVPEITSSSHOHPVKTLGSLDAFMIINSPDPVPSRRSIF 261
DB 243 FTFOALLMDGRIIFGYKEIPVLVTQISSTNHPKVLGSLDAFVVMHRTQIQIPNVRRTIY 302
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262 EYHRIELDPKSVTSMASVEFTPLPTCLQHRSCDAMSSDLTFNCSWCHVLCRCSSGPDY 321
DB 303 EYHVELQMSKITNISAVEMTPLTCLQFNGCGPSSQIGFNCWSCKLQRCSSGPDYH 362

QY 322 ROEWMDYCCAQEAG--RMCEDFQDEHDHDSASPTSPSYDGLTTS----SSLFIDSL 375
DB 363 RQDWDVSGCPPEVQSKMKCEKTBPGETSTQTTTSHTTMOFRVLTTTTRRAVTSOMPTSL 422

QY 376 TTEDDTKLNPYAGGDLQ--NNLSPKTKGTPVHLGTI 410
DB 423 PTEDDTKLALHDKDSGASTDSDAAEKKGGTLHAGLI 458

RESULT 12
Q9DC11 PRELIMINARY; PRT; 530 AA.
AC Q9DC11;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Mus musculus adult male lung cDNA, RIKEN full-length enriched library,
clone:1200007L24 product:TUMOR ENDOTHELIAL MARKER 7-RELATED
DE homolog.
GN Name=Plxdc2;
OS Mus musculus (Mouse).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RA "High-efficiency full-length cDNA cloning."
EL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection."
EL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RA The FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs."
EL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes."
EL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagasaka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Villalon D.K., Muzny K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Richards S., Worley K.C., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Touchman J.W., Green E.D., Dickinson M.C.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RA "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RN SEQUENCE FROM N.A.  
RP STRAIN=NMRI; TISSUE=Mammary tumor;  
RC Strausberg R.;  
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC057881; AA457881.1; -;  
SQ SEQUENCE 530 AA; 59646 MW; D7256C02073417FC CRC64;  
Query Match 47.1%; Score 1044; DB 2; Length 530;  
Best Local Similarity 51.3%; Pred. No. 2.7e-77;  
Matches 203; Conservative 67; Mismatches 112; Indels 14; Gaps 6;  
QY 27 WNRARSPGHVSEPDRTQISQ-----DLGGTGLAMDTLPDNRTRVED-NHSYVYVRLYGPSEP 81  
DB 65 WKRNIV--DPFKAVDTNRASMGQASPEKSGFTDLLLDGQDNNTQIEEDTDHNYISRIY 122  
QY 82 PSEPHSELVDVAENRSQVKIHTILSNTHRQASRVVLSFDFPPYGHPLRQITATGGF 141  
DB 123 PADSASRLWNIDOMEKQVKIHTILSNTHRQARVNLSPDFPFGHFLNEVATGGF 182  
QY 142 IFMGDVIHRLMTATQYVAPLMANFNPGVSDNSTVYFDNGTVFVQMDHVLQDNYLGS 201  
DB 183 IYGEVVRHRLMTATQYVAPLMANFNPDPSVRNSTVYFDNGTVFVQMDHVLQDNYLGS 242  
QY 202 FTFOALHHDGRIVFAYKEIPMSVPEISSQHPVKTGLSDAFMILNPSDPVPSRRRSIF 261  
DB 243 FTFOATLLMDGRIFGYKEIPVLVTQISSTNHPVKVGLSDAFVVRHRIQIIPNRRRTIV 302  
QY 262 EYHRIELDPKVTSMASVEFTPLTCLQHRSCDMSDLTFNCSWCHVLRQCSGGFDY 321  
DB 303 EYHRIELQMSKITNISAVEMTPLTCLQFNGCGPCVSSQIGFNCSCWCKLQRCSSGFDH 362  
QY 322 ROEMMDYGCQAQAEAG--RMCEDFODEDHDSDASPDTSFSDYDGLTTTS----SSLFTDSL 375  
DB 363 RQMDVDSGCCPEEVOSKEMKEKTEPGTSTQTTTSHHTTQWFRVLTTRRAVTSQMPTSL 422  
QY 376 TTEDDTKLNPYAGDGLQ--NNLSPKTKGTPVHLGTI 410  
DB 423 PTEDDTKLALHDKSGASTDSDSAEKKGGTLHAGLI 458  
RESULT 15  
Q6DE92  
ID Q6DE92 PRELIMINARY; PRY; 513 AA.  
AC Q6DE92;  
DT 01-OCT-2004 (TrEMBLrel. 28, Created)  
DT 01-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Hypothetical protein.  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8355;

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Villalon D.K., Muzny K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Richards S., Worley K.C., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Touchman J.W., Green E.D., Dickinson M.C.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RA "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [3]  
RN SEQUENCE FROM N.A.  
RP TISSUE=Ovary;  
RC Klein S., Strausberg R.;  
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC077242; AAH77242.1; -;  
KW Hypothetical protein.  
SQ SEQUENCE 513 AA; 57622 MW; 301EA53F2905A4ED CRC64;  
Query Match 46.6%; Score 1034.5; DB 2; Length 513;  
Best Local Similarity 51.3%; Pred. No. 1.6e-76;  
Matches 200; Conservative 69; Mismatches 106; Indels 15; Gaps 5;  
QY 27 WNRARSPGHVSEPDRTQISQDLGGTGLAMDTLPDNRTRVED-NHSYVYVRLYGPSEP 85  
DB 61 WKQSVDT-----NRPSVGQDF--PDMFLEGTNENGTEIEDTDHRYTSRYGPDLS 111  
QY 86 HSRELWVDVAENRSQVKIHTILSNTHRQASRVVLSFDFPPYGHPLRQITATGGFIMG 145  
DB 112 ASRDLWNIDOMEKQVKIHTILSNTHRQARVNLSPDFPFGHFLNEVATGGFIYTG 171  
QY 146 DVTHRLMTATQYVAPLMANFNPGVSDNSTVYFDNGTVFVQMDHVLQDNYLGSFTFQ 205  
DB 172 EVVRHRLMTATQYVAPLMANFNPDPSVRNSTVYFDNGTVFVQMDHVLQDNYLGSFTFQ 231  
QY 206 AALHHDGRIVFAYKEIPMSVPEISSQHPVKTGLSDAFMILNPSDPVPSRRRSIFEYHR 265  
DB 232 ATLINDGRIVFGYKIDIPVQVQISSTNHPVKVGLSDAFVVRHRIQIIPNRRRTIFEYHR 291  
QY 266 IELDPKVTSMASVEFTPLTCLQHRSCDMSDLTFNCSWCHVLRQCSGGFDYRQEW 325  
DB 292 VELEMTKITSFSAVEMLPLATCLQFNCSSCVSMIGFNCSCWCIPORCSSGGFDRHQDW 351  
QY 326 MDYGCQAQAEGRMCEDPDQ-----EDHDSASPDTSFSDYDGLTTTSSSLFIDSITTEDDT 381  
DB 352 VENGTEESKDTVCDDLLQTTIGISHHTTGLHATTSTIYAFTTTTTMRASHFPNLTEDDT 411  
QY 382 KLNPYAGDGLQ--NNLSPKTKGTPVHLGTI 410  
DB 412 KIALHLKNDGASTDSDSAEKKGGTLHAGLI 441

Search completed: January 28, 2005, 22:11:23  
Job time : 141.695 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 28, 2005, 21:55:21 ; Search time 22.1468 Seconds  
(without alignments)  
1688.701 Million cell updates/sec

Title: US-09-918-715-230\_COPY\_280\_344

Perfect score: 370

Sequence: 1 YHRIEPLPSKVTSMASVEFT.....CHVLQRCSGFDYRQEWMD 65

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot\_02.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	370	100.0	500	2	Q8IUK5
2	370	100.0	500	2	Q9HCT9
3	325	87.8	500	2	Q9CWW5
4	325	87.8	500	2	Q91ZV7
5	325	87.8	507	2	Q8BM20
6	287	77.6	351	2	Q8ZSC8
7	287	77.6	351	2	BAC87025
8	264	71.4	530	2	Q6PET5
9	264	71.4	530	2	Q9DC11
10	264	71.4	530	2	Q91ZV6
11	264	71.4	530	2	AAH57881
12	263	71.1	480	2	Q96E59
13	263	71.1	529	2	Q6UX71
14	263	71.1	529	2	Q96PD9
15	263	71.1	529	2	AAQ88850
16	251	67.8	513	2	Q6DE92
17	172	46.5	625	2	Q9W2V9
18	137	37.0	498	2	Q18500
19	101	27.3	1568	2	Q60486
20	100.5	27.2	384	2	Q7Q2J8
21	90.5	24.5	2119	2	Q8CJH3
22	84	22.7	1764	2	Q45657
23	84	22.7	1764	2	CAB05755
24	83.5	22.6	729	2	Q9UJ93
25	83.5	22.6	835	2	Q6DCP0
26	83.5	22.6	1832	2	Q6NY20
27	83.5	22.6	1832	2	AAH66773
28	83.5	22.6	1952	2	Q9UJ92
29	83.5	22.6	2135	2	Q9UIV7
30	83.5	22.6	2143	2	Q43157
31	82.5	22.3	506	2	P90641

32	82	22.2	749	2	Q8C3X9
33	82	22.2	1205	2	Q8CGW1
34	82	22.2	1574	2	Q9QZC2
35	81	21.9	190	2	Q86E23
36	81	21.9	343	2	Q6PVY2
37	81	21.9	343	2	AA68255
38	80.5	21.8	1871	1	FLX4_HUMAN
39	80	21.6	1328	2	Q9UIW1
40	80	21.6	1384	2	Q76915
41	80	21.6	1384	2	BAD05055
42	80	21.6	1963	2	Q75051
43	77.5	20.9	1872	2	P70208
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45	76	20.5	676	2	Q6YBW0

## ALIGNMENTS

RESULT 1

Q8IUK5 PRELIMINARY; PRT; 500 AA.

AC Q8IUK5;

DT 01-MAR-2003 (TREMBlrel. 23, Created)

DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)

DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)

DE Plexin domain containing 1.

GN Name=PLXDC1;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Testis;

RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.F., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,

RA Jones S.J., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences."

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

R2 SEQUENCE FROM N.A.

RP TISSUE=Testis;

RC Strausberg R.;

RA Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC036059; AAH36059.1; -.

DR Genew; HGNC:20945; PLXDC1.

DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0004872; F:receptor activity; IEA.

DR GO; GO:0007275; P:development; IEA.

DR InterPro; IPR003659; Plexin-like.

DR Pfam; PF01437; PSI; 1.

DR SMART; SM00423; PSI; 1.

SQ SEQUENCE 500 AA; 55778 MW; 3FA4F9D98A514ABF CRC64;

Query Match 100.0%; Score 370; DB 2; Length 500;





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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ON NCBI_TaxID=9606;
RX [1]
RN
RP SEQUENCE FROM N.A.
RA Oshina A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K.,
RA Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Umezawa A., Imabayashi H.,
RA Fukuma M., Hata J., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y.,
RA Saito K., Nishikawa T., Kimura K., Yamashita H., Matsuoka K.,
RA Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
RA Murakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y.,
RA Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK127539; BAC87025.1; -
SQ SEQUENCE 351 AA, 39639 MW; PF03CC9D78E4604A CRC64;

Query Match 77.6%; Score 287; DB 2; Length 351;
Best Local Similarity 91.2%; Pred. No.1.5e-25;
Matches 52; Conservative 1; Mismatches 4; Indels 0; Gaps

Qy 1 YHRIELDPKSVTMSAVSFPLPTCLOHRSQCDACMSSDLTFNCSWCHVLQRCSSGPD 57
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Db 273 YHRIELDPKSVTMSAVSFPLPTCLOHRSQCDACMSSDLTFNCSWCHVLQRCSSGPD 329
|||

RESULT 8
Q6PETS PRELIMINARY; PRT; 530 AA.
ID AC Q6PETS5
IC Q6PETS5
AD Q6PETS5
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Tumor endochelial marker 7-related.
GN Names=Plxdc2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON NCBI_TaxID=10090;
RX [1]
RN
RP SEQUENCE FROM N.A.
RA STRAIN=NNRI; TISSUE=Mammary tumor. WAP-Tag model. 5 months old;
RC MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.W., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywicki M.I., Skalska U., Smallos D.B., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RX [2]
RN
RP SEQUENCE FROM N.A.
RA STRAIN=NNRI; TISSUE=Mammary tumor. WAP-Tag model. 5 months old;
RC Strausberg R.;
RA Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC057881; AAHS7881.1; -
DR InterPro; IPR003659; Plexin-like.
DR InterPro; IPR002165; Plexin repeat.

```





[illegible]

05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE ARFP2514.  
 GN ORFNames=UNQ2514;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22887296; PubMed=12975309;  
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,  
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,  
 RA Eaton D., Foster J., Grimaldi C., Gu Q., Haas P.E., Heldens S.,  
 RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,  
 RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,  
 RA Seehagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,  
 RA Vandlen R., Watanabe C., Wiedand D., Woods K., Xie M.H., Yaneura D.,  
 RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,  
 RA Godowski P.;  
 RT "The secreted protein discovery initiative (SPDI), a large-scale  
 RT effort to identify novel human secreted and transmembrane proteins: a  
 RT bioinformatics assessment.";  
 RL Genome Res. 13:2265-2270(2003).  
 DR EMBL; AY358486; AAQ88850.1; -.  
 DR InterPro; IPR003659; Plexin-like.  
 DR InterPro; IPR002165; Plexin\_repeat.  
 DR Pfam; PF01437; PSI; 1.  
 DR SMART; SM00423; PSI; 1.  
 SQ SEQUENCE 529 AA; 59583 MW; CCE911D6DF837B40 CRC64;  
 Query Match 71.1%; Score 263; DB 2; Length 529;  
 Best Local Similarity 67.7%; Pred. No. 1.5e-22;  
 Matches 44; Conservative 9; Mismatches 12; Indels 0; Gaps 0;  
 Qy 1 YHRIELDPKVTSMASAVEFTPLPTCLQHRSCDACMSSDLTFCNSCHVLCRCSSGFDRYR 60  
 Db 304 YHRVELQMSKITNISAVEMTFLPTCLQPNRCPCVSSQIGFNCSCWCKLQRCSSGFDRHR 363  
 Qy 61 QEWMND 65  
 Db 364 QDWVD 368  
 RESULT 14  
 ID Q96PD9 PRELIMINARY; PRT; 529 AA.  
 AC Q96PD9;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Tumor endothelial marker 7-related precursor.  
 GN Name=TM7R;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21443268; PubMed=11559528;  
 RA Carson-Walter E.B., Watkins D.N., Nanda A., Vogelstein B.,  
 RA Kinzler K.W., St Croix B.;  
 RT "Cell surface tumor endothelial markers are conserved in mice and  
 RT humans.";  
 RL Cancer Res. 61:6649-6655(2001).  
 DR EMBL; AF378757; AALJ1994.1; -.  
 DR Genew; HGNC:21013; FLXDC2.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0007275; P:development; IEA.  
 DR InterPro; IPR003659; Plexin-like.  
 DR InterPro; IPR002165; Plexin\_repeat.  
 DR Pfam; PF01437; PSI; 1.  
 DR SMART; SM00423; PSI; 1.

KW Signal.  
 FT SIGNAL 1 30 Potential.  
 FT CHAIN 31 529 tumor endothelial marker 7-related.  
 SQ SEQUENCE 529 AA; 59583 MW; D44A0975DF894840 CRC64;  
 Query Match 71.1%; Score 263; DB 2; Length 529;  
 Best Local Similarity 67.7%; Pred. No. 1.5e-22;  
 Matches 44; Conservative 9; Mismatches 12; Indels 0; Gaps 0;  
 Qy 1 YHRIELDPKVTSMASAVEFTPLPTCLQHRSCDACMSSDLTFCNSCHVLCRCSSGFDRYR 60  
 Db 304 YHRVELQMSKITNISAVEMTFLPTCLQPNRCPCVSSQIGFNCSCWCKLQRCSSGFDRHR 363  
 Qy 61 QEWMND 65  
 Db 364 QDWVD 368  
 RESULT 15  
 ID AAQ88850 PRELIMINARY; PRT; 529 AA.  
 AC AAQ88850;  
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)  
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)  
 DE ARFP2514.  
 GN UNQ2514.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX PubMed=12975309;  
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,  
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,  
 RA Eaton D., Foster J., Grimaldi C., Gu Q., Haas P.E., Heldens S.,  
 RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,  
 RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,  
 RA Seehagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,  
 RA Vandlen R., Watanabe C., Wiedand D., Woods K., Xie M.H., Yaneura D.,  
 RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,  
 RA Godowski P.;  
 RT "The Secreted Protein Discovery Initiative (SPDI), a Large-Scale  
 RT Effort to Identify Novel Human Secreted and Transmembrane Proteins: A  
 RT Bioinformatics Assessment.";  
 RL Genome Res. 13:2265-2270(2003).  
 DR EMBL; AY358486; AAQ88850.1; -.  
 SQ SEQUENCE 529 AA; 59583 MW; CCE911D6DF837B40 CRC64;  
 Query Match 71.1%; Score 263; DB 2; Length 529;  
 Best Local Similarity 67.7%; Pred. No. 1.5e-22;  
 Matches 44; Conservative 9; Mismatches 12; Indels 0; Gaps 0;  
 Qy 1 YHRIELDPKVTSMASAVEFTPLPTCLQHRSCDACMSSDLTFCNSCHVLCRCSSGFDRYR 60  
 Db 304 YHRVELQMSKITNISAVEMTFLPTCLQPNRCPCVSSQIGFNCSCWCKLQRCSSGFDRHR 363  
 Qy 61 QEWMND 65  
 Db 364 QDWVD 368  
 Search completed: January 28, 2005, 22:11:21  
 Job time : 23.1468 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 28, 2005, 21:55:58 ; Search time 4.50139 Seconds  
(without alignments)  
1389.370 Million cell updates/sec

Title: US-09-918-715-230\_COPY\_280\_344  
Perfect score: 370  
Sequence: 1 YHRIELDPKVTSMASVEFT.....CHVLQRCSGFDYRQEWMD 65  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR.79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	137	37.0	476	2 T19786	hypothetical prote
2	101	27.3	1568	2 T09074	semaphorin recepto
3	84	22.7	1806	2 T32298	hypothetical prote
4	77.5	20.9	1872	2 JC4976	plexin 3 precursor
5	76.5	20.7	1905	2 T51553	Plexin - African c
6	76	20.5	1884	2 JC4975	plexin 2 precursor
7	75	20.3	1945	2 T13937	plexin A - fruit f
8	74	20.0	1894	2 JC4980	plexin 1 precursor
9	70	18.9	1379	1 S01254	hepatocyte growth
10	69.5	18.8	465	2 D88448	protein C45G9.8 [i
11	69	18.6	444	2 G84565	probable flavonol
12	68	18.4	1390	1 TVHUME	hepatocyte growth
13	67.5	18.2	1375	2 T30813	plasminogen relate
14	67.5	18.2	2051	2 T13164	plexin B - fruit f
15	67	18.1	174	2 G81349	periplasmic nitrat
16	67	18.1	1375	1 JC5148	hepatocyte growth
17	65	17.6	1425	2 T30811	hepatocyte growth
18	64.5	17.4	413	2 H75070	sugar-phosphate nu
19	64.5	17.4	1291	2 T21694	hypothetical prote
20	64	17.3	470	2 H84565	probable flavonol
21	63.5	17.2	846	2 A30899	integrin beta chai
22	63	17.0	1404	1 A48196	protein-tyrosine k
23	62.5	16.9	439	2 S33293	testican - human
24	62.5	16.9	491	2 S31784	vps protein - bovi
25	62.5	16.9	712	2 T27165	hypothetical prote
26	62.5	16.9	774	2 G71308	probable aminopept
27	62.5	16.9	1042	2 T16169	hypothetical prote
28	61	16.5	210	2 S76973	hypothetical prote
29	61	16.5	3938	2 T42761	Bassoon protein -

30 Bassoon protein -  
31 hypothetical prote  
32 hypothetical conse  
33 hypothetical prote  
34 hypothetical prote  
35 probable membrane  
36 protein-tyrosine k  
37 protein F3M18.14 [i  
38 probable SET-domai  
39 hypothetical prote  
40 salivary protein 1  
41 probable zinc fing  
42 hypothetical prote  
43 probable sugar-pho  
44 probable C2H2-type  
45

61 16.5 3942 2 T42730  
60 16.2 90 2 S70194  
60 16.2 245 2 E95974  
60 16.2 548 2 T16642  
59.5 16.1 513 2 T33512  
59.5 16.1 543 2 S64850  
59.5 16.1 1621 2 T30200  
59.5 16.1 1819 2 E86410  
59 15.9 338 2 T26588  
59 15.9 447 2 T00834  
59 15.9 555 2 T23531  
58.5 15.8 311 2 S08110  
58.5 15.8 362 2 E86382  
58.5 15.8 397 2 T08345  
58.5 15.8 416 2 A71095  
58.5 15.8 439 2 A84431

ALIGNMENTS

RESULT 1  
T19786  
hypothetical protein C36E8.3 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T19786

R;Wilkinson, J.; Barlow, K.  
Submitted to the EMBL Data Library, August 1994

A;Reference number: Z19177  
A;Accession: T19786  
A;Status: preliminary; translated from GB/EMBL/DBDJ

A;Molecule type: DNA

A;Residues: 1-476 <WIL>

A;Cross-references: UNIPROT:Q18500; EMBL:Z35597; PIDN:CAA84646.1; GSPDB:GN00021; CESP:C36E8

A;Experimental source: clone C36E8

C;Genetics:

A;Gene: CESP:C36E8.3

A;Map position: 3

A;Introns: 23/1; 101/3; 152/3; 206/3; 235/1; 255/3; 320/1; 445/2

C;Superfamily: Caenorhabditis elegans hypothetical protein C36E8.3

Query Match 37.0%; Score 137; DB 2; Length 476;  
Best Local Similarity 37.0%; Pred. No. 8.4e-08;  
Matches 27; Conservative 11; Mismatches 27; Indels 8; Gaps 3;  
Qy 1 YHRIELDPKVTSMASVEFTPLPTCLOHRSQCDACMSSDLT-FNCSWCHVLQR-----CS- 53  
Db 297 YHRIETAAQKIVSNTVILKQAQPTCTISFDCTCTNATLPHFNCLWCHAKKSHGGPFCTD 356

Qy 54 -SGFDYRQEWMD 65

Db 357 EAGLHRRRQHWFE 369

RESULT 2

T09074  
semaphorin receptor VESPR - human

C;Species: Homo sapiens (man)

C;Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004

C;Accession: T09074

R;Comeau, M.R.; Johnson, R.; DuBoise, R.F.; Petersen, M.; Geating, P.; van den Bos, T.; P

Immunity 8, 473-482, 1998

A;Title: A poxvirus-encoded semaphorin induces cytokine production from monocytes and bi

A;Reference number: Z16555; MUID:98246049; PMID:9586637

A;Accession: T09074

A;Status: preliminary; translated from GB/EMBL/DBDJ

A;Molecule type: mRNA

A;Residues: 1-1568 <COM>

A;Cross-references: UNIPROT:O60486; EMBL:AF030339; NID:g3176761; PIDN:AAC18823.1; PID:g3

A;Experimental source: tissue type foreskin; cell type fibroblast

C;Genetics:

A;Gene: VESPR



C;Genetics:  
A;Gene: plexA  
A;Cross-references: FlyBase:FBgn0025741  
A;Map position: 4  
C;Function:  
A;Description: may function as repellents during axon guidance  
C;Keywords: cell adhesion; nerve

Query Match 20.3%; Score 75; DB 2; Length 1945;  
Best Local Similarity 44.8%; Pred. No. 2.7;  
Matches 13; Conservative 3; Mismatches 11; Indels 2; Gaps 1;

Qy 25 CLQHRSCDACMSSDLTFNCSWCHVLQRC 53  
Db 672 CSTHSSCTRCVSSS--FPDCMVCVAHRCT 698

RESULT 8  
JC4980  
plexin 1 precursor - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 31-Dec-1996 #sequence\_revision 31-Dec-1996 #text\_change 09-Jul-2004  
C;Accession: JC4980  
R;Kameyama, T.; Murakami, Y.; Suto, F.; Kawakami, A.; Takagi, S.; Hirata, T.; Fujisawa, Biochem. Biophys. Res. Commun. 226, 524-529, 1996  
A;Title: Identification of a neuronal cell surface molecule, plexin, in mice.  
A;Reference number: JC4980; MUID:96400291; PMID:8806667  
A;Accession: JC4980  
A;Status: nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-1894 <KAM>  
A;Cross-references: UNIPROT:P70206; DBJ:D86948; NID:gl65756; PIDN:BAA13188.1; PID:d101  
A;Experimental source: brain  
C;Comment: This protein is a membrane protein, and plays a role in neuronal cell contact  
ence of calcium ions.  
C;Keywords: duplication; transmembrane protein  
F;1-22/Domain: signal sequence #status predicted <SIG>  
F;513-561/Domain: 659-704, 807-859/Region: cysteine-rich  
F;1238-1264/Domain: transmembrane #status predicted <TMM>  
F;1266-1268/Region: hydrophilic

Query Match 20.0%; Score 74; DB 2; Length 1894;  
Best Local Similarity 44.0%; Pred. No. 3.4;  
Matches 11; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

Qy 29 RSCDACMSSDLTFNCSWCHVLQRC 53  
Db 812 QSCGLCLKADPRFCGVCVAERCS 836

RESULT 9  
S01254  
hepatocyte growth factor receptor precursor - mouse  
N;Contains: protein-tyrosine kinase (EC 2.7.1.112) met  
C;Species: Mus musculus (house mouse)  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C;Accession: S01254; JH0115; A4543  
R;Chan, A.M.L.; King, H.W.S.; Deakin, E.A.; Tempest, P.R.; Hilkens, J.; Kroezen, V.; Edw  
Oncogene 2, 593-599, 1988  
A;Title: Characterization of the mouse met proto-oncogene.  
A;Reference number: S01254; MUID:88262253; PMID:2838789  
A;Accession: S01254  
A;Molecule type: mRNA  
A;Residues: 1-1379 <CHA>  
A;Cross-references: UNIPROT:P16056; EMBL:Y00671; NID:g53058; PIDN:CAA68680.1; PID:g53059  
R;Wilks, A.F.; Kurban, R.R.; Hovens, C.M.; Ralph, S.J.  
Gene 85, 67-74, 1989  
A;Title: The application of the polymerase chain reaction to cloning members of the prot  
A;Reference number: JH0112; MUID:90152381; PMID:2482828  
A;Accession: JH0115  
A;Molecule type: mRNA  
A;Residues: 'I', 1200-1254, 'R', 1256-1260, 'T', 1262-1268 <WIL>  
A;Experimental source: hemopoietic cell

A;Note: the authors translated the codon ACG for residue 1261 as Lys  
R;Weidner, K.M.; Sachs, M.; Birchmeier, W.  
J. Cell Biol. 121, 145-154, 1993  
A;Title: The Met receptor tyrosine kinase transduces motility, proliferation, and morpho  
A;Reference number: A45453; MUID:93209981; PMID:8384622  
A;Accession: A45453  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: mRNA  
C;Genetics:  
A;Gene: met  
C;Superfamily: hepatocyte growth factor receptor; protein kinase homology  
C;Keywords: ATP; autophosphorylation; glycoprotein; phosphoprotein; phosphotransferase;  
F;1-24/Domain: signal sequence #status predicted <SIG>  
F;25-929/Domain: extracellular #status predicted <EXT>  
F;25-302/Product: hepatocyte growth factor receptor alpha chain #status predicted <ACH>  
F;308-1379/Product: hepatocyte growth factor receptor beta chain #status predicted <BCH>  
F;930-954/Domain: transmembrane #status predicted <TMM>  
F;955-1379/Domain: intracellular #status predicted <INT>  
F;1074-1342/Domain: protein kinase homology <KIN>  
F;1082-1090/Region: protein kinase ATP-binding motif  
F;1108/Active site: Lys #status predicted  
F;1233/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predict

Query Match 18.9%; Score 70; DB 1; Length 1379;  
Best Local Similarity 30.4%; Pred. No. 7.2;  
Matches 14; Conservative 5; Mismatches 19; Indels 8; Gaps 2;

Qy 18 EFTPLPT----CLQHRSCDACMSSDLTFNCSWCH----VLQRCSSG 55  
Db 508 KITKIPLNGLCGHFQSCQLSAPYFIQCWCHNQCRFDECPSG 553

RESULT 10  
D88448  
protein C45G9.8 [imported] - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004  
C;Accession: D88448  
R;anonymous, The C. elegans Sequencing Consortium.  
Science 282, 2012-2018, 1998  
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog  
A;Reference number: A75000; MUID:99089613; PMID:9851916  
A;Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C\_ele  
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and  
A;Accession: D88448  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-465 <STO>  
A;Cross-references: UNIPROT:Q09280; GB:chr\_III; PIDN:AAA62551.1; PID:g687873; GSPDB:GN00  
C;Genetics:  
A;Gene: C45G9.8  
A;Map position: 3

Query Match 18.8%; Score 69.5; DB 2; Length 465;  
Best Local Similarity 30.0%; Pred. No. 3.1;  
Matches 18; Conservative 10; Mismatches 31; Indels 1; Gaps 1;

Qy 3 RIELDSKVTMSGAVETPLPTCLQHRSCDACMSSDLTFNCSWCHVLQRCSSGFDYRQE 62  
Db 56 RMQIDRLRRSTEHVEIVPOETCVHHESPDVLTFCATMSTS-THVMNPSSTISKGATE 114

RESULT 11  
G84565  
probable flavonol 3-O-glucosyltransferase [imported] - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
C;Accession: G84565  
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vautken, S.E.; Unayam, L.; Tallon, L.  
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J  
Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A;Reference number: A84420; MUID:20083487; PMID:10617197  
A;Accession: G84565  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-444 <S>  
A;Cross-references: UNIPROT:Q9ZU71; GB:AE002093; NID:G4218003; PIDN:AA012211.1; GSPDB:GN  
C;Genetics:  
A;Gene: At2g18560  
A;Map position: 2  
C;Superfamily: flavonol O3-glucosyltransferase

Query Match 18.6%; Score 69; DB 2; Length 444;  
Best Local Similarity 24.6%; Pred. No. 3.4; Mismatches 26; Indels 10; Gaps 2;  
Matches 16; Conservative 13

Qy 6 LDPKSVTMSAVEPTPLPTCLQHRSCDACMSDDLTFNCSCWCHVLQRCSSG-----FDRYR 60  
Db LDRTRGVGLVVTQWAPQVEILSHRSIGGFLS-----HCGWSSVLESITKGVPIIAWPLYA 357  
Qy 61 QEWMD 65  
Db 358 EQWMN 362

RESULT 12  
TVRUME  
hepatocyte growth factor receptor precursor - human  
N;Contains: protein-tyrosine kinase (SC 2.7.1.112) met  
C;Species: Homo sapiens (man)  
C;Date: 31-Mar-1991 #sequence revision 30-Sep-1992 #text change 09-Jul-2004  
C;Accession: A40175; A28303; A93749; A93369; A53761; 157632; A30008; B24569  
R;Giordano, S.  
submitted to the EMBL Data Library, November 1990  
A;Reference number: A40175  
A;Accession: A40175  
A;Molecule type: mRNA  
A;Residues: 1-1390 <GIO>  
A;Cross-references: UNIPROT:P08581; EMBL:X54559  
R;Park, M.; Dean, M.; Kaul, K.; Braun, M.J.; Gonda, M.A.; Vande Woude, G.  
Proc. Natl. Acad. Sci. U.S.A. 84, 6379-6383, 1987  
A;Title: Sequence of MET protooncogene cDNA has features characteristic of the tyrosine  
A;Reference number: A28303; MUID:87317655; PMID:2819873  
A;Accession: A28303  
A;Molecule type: mRNA  
A;Residues: 1-755; 'TWKBPNTVSLFPCFAS', 756-1190, 'A', 1192-1390 <PAR>  
A;Cross-references: GB:J02958; NID:g187558; PIDN:AAA59591.1; PID:g307196  
R;Chan, A.M.L.; King, H.W.S.; Tempest, P.R.; Deakin, E.A.; Cooper, C.S.; Brookes, P.  
Oncogene 1, 229-233, 1987  
A;Title: Primary structure of the met protein tyrosine kinase domain.  
A;Reference number: A93749; MUID:88143699; PMID:3325883  
A;Accession: A93749  
A;Molecule type: mRNA  
A;Residues: 'VNEYRECQSLRLKLNQKALTEKNELEIAQDRNIAIQSQ', 'FTRTKEELEAEKRDILRTNRLSQLEY  
A;Cross-references: GB:U08818; NID:g487741; PIDN:AA860323.1; PID:g487742  
A;Note: this activated met oncogene is the product of gene rearrangement  
R;Dean, M.; Park, M.; Le Beau, M.W.; Robins, T.S.; Diaz, M.O.; Rowley, J.D.; Blair, D.G.  
Nature 318, 385-388, 1985  
A;Title: The human met oncogene is related to the tyrosine kinase oncogenes.  
A;Reference number: A93369; MUID:86065462; PMID:4069211  
A;Accession: A93369  
A;Molecule type: DNA  
A;Residues: 1267-1390 <DEA>  
A;Cross-references: GB:M35074; NID:g187555; PIDN:AAA59590.1; PID:g386868  
R;Gambartota, G.; Pistoi, S.; Giordano, S.; Comoglio, P.M.; Santoro, C.  
J. Biol. Chem. 269, 12852-12857, 1994  
A;Title: Structure and inducible regulation of the human MET promoter.  
A;Reference number: A53761; MUID:94230365; PMID:8175700  
A;Accession: A53761  
A;Molecule type: mRNA  
A;Residues: 1-14 <GAM>  
R;Ferracini, R.; Longati, P.; Naldini, L.; Vigna, E.; Comoglio, P.M.  
J. Biol. Chem. 266, 19558-19564, 1991

A;Title: Identification of the major autophosphorylation site of the Met/hepatocyte growth  
A;Reference number: A40179; MUID:32011756; PMID:1655790  
A;Contents: annotation; autophosphorylation site  
R;Dean, M.; Park, M.; Vande Woude, G.F.  
Mol. Cell. Biol. 7, 921-924, 1987  
A;Title: Characterization of the rearranged tpr-met oncogene breakpoint.  
A;Reference number: 157632; MUID:87144265; PMID:3821733  
A;Accession: 157632  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 963-1009 <RES>  
A;Cross-references: GB:M15325; NID:g187531; PIDN:AAA59585.1; PID:g187532  
C;Comment: The receptor is a dimer of disulfide-bonded 50K alpha and 145K beta chains th  
C;Genetics:  
A;Gene: GDB:MET  
A;Cross-references: GDB:120178; OMIM:164860  
A;Map position: 7q31-q31  
C;Superfamily: hepatocyte growth factor receptor; protein kinase homology  
C;Keywords: ATP; autophosphorylation; glycoprotein; phosphoprotein; phosphotransferase; i  
F;1-24/Domain: signal sequence #status predicted <SIG>  
F;25-303/Product: hepatocyte growth factor receptor alpha chain #status predicted <ALP>  
F;308-1390/Product: hepatocyte growth factor receptor beta chain #status predicted <BET>  
F;933-955/Domain: transmembrane #status predicted <TMN>  
F;1076-1344/Domain: protein kinase homology <KIN>  
F;1084-1092/Region: protein kinase ATP-binding motif  
F;45,106,149,202,399,405,635,785,930/Binding site: carbohydrate (Asn) (covalent) #status  
F;1110/Active site: Lys #status experimental  
F;1235/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status experim

Query Match 18.4%; Score 68; DB 1; Length 1390;  
Best Local Similarity 30.4%; Pred. No. 12;  
Matches 14; Conservative 6; Mismatches 18; Indels 8; Gaps 2;

Qy 18 EFTPLPT-----CLQHRSCDACMSDDLTFNCSCWCH-----VLQRCSSG 55  
Db 509 KITKIPLNLGLGRHFCSCQLSAPPFVQCGWCHDKVCRSECLSG 554

RESULT 13  
T30813  
plasmaingen related growth factor receptor 2 - Fugu rubripes  
C;Species: Fugu rubripes  
C;Date: 02-Sep-2000 #sequence\_revision 02-Sep-2000 #text\_change 09-Jul-2004  
C;Accession: T30813  
R;Cottage, A.J.; Clark, M.; Hawker, K.; Umrana, Y.; Wheller, D.; Bishop, M.; Elgar, G.  
FEBS Lett. 443, 370-374, 1999  
A;Title: Three receptor genes for plasmaingen related growth factors in the genome of th  
A;Reference number: Z20880; MUID:99148833; PMID:10025966  
A;Accession: T30813  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-1375 <COT>  
A;Cross-references: UNIPROT:Q9VGM5; EMBL:AJ010348; NID:e1355080; PID:e1355082; PIDN:CAAO  
C;Genetics:  
A;Gene: PRGR2  
A;Introns: 400/3; 459/3; 499/3; 556/3; 611/2; 655/3; 701/2; 761/2; 794/3; 870/3; 919/3;  
C;Superfamily: hepatocyte growth factor receptor; protein kinase homology

Query Match 18.2%; Score 67.5; DB 2; Length 1375;  
Best Local Similarity 32.4%; Pred. No. 14;  
Matches 12; Conservative 4; Mismatches 14; Indels 7; Gaps 1;

Qy 10 KVTSMGAVEPTPLPTCLQHRSCDACMSDDLTFNCSCW 46  
Db 502 KVPVSLG-----PGCAHFRTCSMCLMAPRFMNCWC 531

RESULT 14  
T13164  
plexin B - fruit fly (Drosophila melanogaster)  
C;Species: Drosophila melanogaster  
C;Date: 13-Aug-1999 #sequence\_revision 13-Aug-1999 #text\_change 09-Jul-2004



C:Accession: T13164  
R:Winberg, M.L.; Noordermeer, J.N.; Tamagnone, L.; Comoglio, P.M.; Spriggs, M.K.; Tessie  
Cell 95, 903-916, 1998  
A:Title: Plexin A is a neuronal semaphorin receptor that controls axon guidance.  
A:Reference number: Z17621; MUID:99091049; PMID:9875845

A:Accession: T13164  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-2051 <MIN>  
A:Cross-references: UNIPROT:O96682; EMBL:AF106933; NID:g4056675; PID:g4056676; PIDN:AA00  
C:Genetics:  
A:Gene: plexB  
A:Cross-references: FlyBase:FBgn0025740  
A:Map position: 4  
C:Function:  
A:Description: plays a role in neuronal cell contact, axon guidance and fasciculation

Query Match 18.2%; Score 67.5; DB 2; Length 2051;  
Best Local Similarity 28.8%; Pred. No.19;  
Matches 15; Conservative 9; Mismatches 23; Indels 5; Gaps 2;

Qy 6 LDPSK---VTMSAVEFTPLPTCLQHRSCDACMSSDLTFNCSWCHVLRCS 53

Db 513 MSPKDFLYVLRSQKIKLRIEHCSTVYNCACLESRDPP-CGWCSLEKRCT 563

## RESULT 15

G81349  
Deripalamic nitrate reductase small chain (cytochrome C-type protein) Cj0783 [imported]  
C:Species: Campylobacter jejuni

C:Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 09-Jul-2004  
C:Accession: G81349  
R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling  
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel  
Nature 403, 665-668, 2000

A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp  
A:Reference number: A81250; MUID:20150912; PMID:10688204

A:Accession: G81349  
A:Status: preliminary  
A:Molecule type: DNA

A:Residues: 1-174 <PAR>  
A:Cross-references: UNIPROT:Q9PPD6; GB:AL139076; GB:AL111168; NID:g6968128; PIDN:CAB7304  
A:Experimental source: serotype O2, strain NCTC 11168

C:Genetics:  
A:Gene: napB; Cj0783  
C:Superfamily: cytochrome c-type protein napB

Query Match 18.1%; Score 67; DB 2; Length 174;  
Best Local Similarity 42.9%; Pred. No. 2.5;  
Matches 15; Conservative 2; Mismatches 14; Indels 4; Gaps 1;

Qy 20 TPLPTC---LQHRSCDACMSSDLTFNCSCWCHVLIQ 50

Db 105 TPLPASHYDFRHNKTTGDMISDRFNCTQCHVPQ 139

Search completed: January 28, 2005, 22:12:42  
Job time : 7.50139 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 28, 2005, 21:59:20 ; Search time 29.518 Seconds  
(without alignments)  
1321.880 Million cell updates/sec

Title: US-09-918-715-230\_COPY\_137\_244

Perfect score: 588

Sequence: 1 LSPDFPYGHLRQITATG.....LHNDGRIVFAYKEIPMSVPE 108

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1608061 seqs, 361289386 residues

Total number of hits satisfying chosen parameters: 1608061

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications AA:\*
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  - 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
  - 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
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  - 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
  - 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
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  - 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
  - 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
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  - 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
  - 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
  - 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
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  - 19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	588	100.0	240	14	US-10-104-047-3712
2	588	100.0	431	10	US-09-912-935-36
3	588	100.0	431	14	US-10-168-365-36
4	588	100.0	488	17	US-10-357-819-4
5	588	100.0	500	10	US-09-918-715-230
6	588	100.0	500	15	US-10-435-696-79
7	588	100.0	500	17	US-10-474-794-230
8	588	100.0	500	17	US-10-357-819-2
9	588	100.0	502	14	US-10-156-487A-5
10	588	100.0	1002	10	US-09-918-715-179
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12	528	89.8	500	10	US-09-918-715-192
13	528	89.8	500	10	US-09-918-715-297

14	528	89.8	500	14	US-10-156-487A-6	Sequence 6, Appli
15	528	89.8	500	17	US-10-474-794-192	Sequence 192, App
16	528	89.8	500	17	US-10-474-794-297	Sequence 297, App
17	417	70.9	392	10	US-09-912-935-23	Sequence 23, Appl
18	417	70.9	392	10	US-09-912-935-25	Sequence 25, Appl
19	417	70.9	392	14	US-10-168-365-23	Sequence 23, Appl
20	417	70.9	392	14	US-10-168-365-25	Sequence 25, Appl
21	417	70.9	425	10	US-09-912-935-35	Sequence 35, Appl
22	417	70.9	425	14	US-10-168-365-35	Sequence 35, Appl
23	417	70.9	449	10	US-09-912-935-34	Sequence 34, Appl
24	417	70.9	449	14	US-10-168-365-34	Sequence 34, Appl
25	417	70.9	499	10	US-09-912-935-31	Sequence 31, Appl
26	417	70.9	499	14	US-10-168-365-31	Sequence 31, Appl
27	417	70.9	529	10	US-09-918-715-189	Sequence 189, App
28	417	70.9	529	10	US-09-918-715-200	Sequence 200, App
29	417	70.9	529	10	US-09-912-935-28	Sequence 28, Appl
30	417	70.9	529	10	US-09-912-935-40	Sequence 40, Appl
31	417	70.9	529	13	US-10-052-586-472	Sequence 472, App
32	417	70.9	529	13	US-10-066-500-128	Sequence 128, App
33	417	70.9	529	14	US-10-174-590-472	Sequence 472, App
34	417	70.9	529	14	US-10-176-758-472	Sequence 472, App
35	417	70.9	529	14	US-10-175-737-472	Sequence 472, App
36	417	70.9	529	14	US-10-174-581-472	Sequence 472, App
37	417	70.9	529	14	US-10-176-483-472	Sequence 472, App
38	417	70.9	529	14	US-10-176-749-472	Sequence 472, App
39	417	70.9	529	14	US-10-176-914-472	Sequence 472, App
40	417	70.9	529	14	US-10-176-915-472	Sequence 472, App
41	417	70.9	529	14	US-10-173-706-472	Sequence 472, App
42	417	70.9	529	14	US-10-175-738-472	Sequence 472, App
43	417	70.9	529	14	US-10-175-752-472	Sequence 472, App
44	417	70.9	529	14	US-10-176-482-472	Sequence 472, App
45	417	70.9	529	14	US-10-176-757-472	Sequence 472, App

ALIGNMENTS

RESULT 1

US-10-104-047-3712  
; Sequence 3712, Application US/10104047  
; Publication No. US20030236392A1  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: No. US20030236392A1el full length cDNA  
; FILE REFERENCE: HI-A0105  
; CURRENT APPLICATION NUMBER: US/10/104,047  
; CURRENT FILING DATE: 2002-03-25  
; PRIOR APPLICATION NUMBER:  
; PRIOR FILING DATE:  
; NUMBER OF SEQ ID NOS: 4096  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 3712  
; LENGTH: 240  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-104-047-3712

Query Match 100.0%; Score 588; DB 14; Length 240;  
Best Local Similarity 100.0%; Pred. No. 1.4e-60;  
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	LSPDFPYGHLRQITATGGFI	MG	DV	IHR	MLT	ATQ	VAP	L	MAN	FPG	YSD	NTSV	V	F	D	60		
Db	64	LSPDFPYGHLRQITATGGFI	MG	DV	IHR	MLT	ATQ	VAP	L	MAN	FPG	YSD	NTSV	V	F	D	123		
Qy	61	NGTVFVQWDHVLYQGWEDK	GS	FT	FQ	AL	HH	DGR	I	V	FAY	KE	I	P	M	S	V	PE	108
Db	124	NGTVFVQWDHVLYQGWEDK	GS	FT	FQ	AL	HH	DGR	I	V	FAY	KE	I	P	M	S	V	PE	171

RESULT 2

US-09-912-935-36  
; Sequence 36, Application US/09912935

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; Publication No. US20030022825A1
; GENERAL INFORMATION:
; APPLICANT: Nishikawa, Mitsuao et al.
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
; FILE REFERENCE: 32066/37483
; CURRENT APPLICATION NUMBER: US/09/912.935
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: PCT/US00/35260
; PRIOR FILING DATE: 2000-12-23
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 36
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-912-935-36

Query Match      100.0%; Score 588; DB 10; Length 431;
Best Local Similarity 100.0%; Pred. No. 2.9e-60;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 NGTVFVQWHDVYVQQWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPE 108
Db 126 NGTVFVQWHDVYVQQWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPE 173

RESULT 3
US-10-168-365-36
; Sequence 36, Application US/10168365
; Publication No. US20030211987A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Childs, John
; APPLICANT: Chao, Cheng-Chi
; APPLICANT: Drmanac, Radoje T
; APPLICANT: Mize, Nancy
; APPLICANT: Lee, Jui
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
; FILE REFERENCE: 30266/37630
; CURRENT APPLICATION NUMBER: US/10/168.365
; CURRENT FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 36
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-168-365-36

Query Match      100.0%; Score 588; DB 14; Length 431;
Best Local Similarity 100.0%; Pred. No. 2.9e-60;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LSPDFPFYGHPLRQITATGTFIFMGDVHHRMLTATQYVAPLMAFNPGYSDNSTVYFD 60
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Qy 61 NGTVFVQWHDVYVQQWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPE 108
Db 126 NGTVFVQWHDVYVQQWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPE 173

RESULT 4
US-10-357-819-4
; Sequence 4, Application US/10357819
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; Publication No. US20040259774A1
; GENERAL INFORMATION:
; APPLICANT: Alvarez, Enrique
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Gorman, Linda
; APPLICANT: Guo, Xiaojia
; APPLICANT: Ji, Weizhen
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Li, Li
; APPLICANT: Miller, Charles E.
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Rastelli, Luca
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-539A
; CURRENT APPLICATION NUMBER: US/10/357.819
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 09/584,411
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 09/783,436
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 10/085,198
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 60/353,301
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 60/355,099
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: 60/356,424
; PRIOR FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: 60/358,239
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: 60/358,608
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/359,367
; PRIOR FILING DATE: 2002-02-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: Curasequest version 0.1
; SEQ ID NO 4
; LENGTH: 488
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-357-819-4

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Best Local Similarity 100.0%; Pred. No. 3.4e-60;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 NGTVFVQWHDVYVQQWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPE 108
Db 197 NGTVFVQWHDVYVQQWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPE 244

RESULT 5
US-09-918-715-230
; Sequence 230, Application US/09918715
; Publication No. US20030017157A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
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; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/09/918,715
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 230
; LENGTH: 500
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-918-715-230

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RESULT 6
US-10-435-696-79
; Sequence 79, Application US/10435696
; Publication No. US20040018525A1
; GENERAL INFORMATION:
; APPLICANT: Wirtz, Ralph
; APPLICANT: Munnes, Marc
; APPLICANT: Kallabis, Harald
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE PREDICTION, DIAGNOSIS, PROGNOSIS
; FILE REFERENCE: LeA 36 108
; CURRENT APPLICATION NUMBER: US/10/435,696
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: EP03003112.4
; PRIOR FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: EP02010291.9
; PRIOR FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 314
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 79
; LENGTH: 500
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-435-696-79

Query Match      100.0%; Score 588; DB 15; Length 500;
Best Local Similarity 100.0%; Pred. No. 3.5e-60;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LSPDFPPYGHPLRQITTIATGCFIFMGDVHHRMLTATQYVAPLMAFNFGYSDNSTVYVFD 60
    |||||
Db 137 LSPDFPPYGHPLRQITTIATGCFIFMGDVHHRMLTATQYVAPLMAFNFGYSDNSTVYVFD 196
    |||||

Qy 61 NGTVFVQWHDVYVQWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPE 108
    |||||
Db 197 NGTVFVQWHDVYVQWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPE 244
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RESULT 7
US-10-474-794-230
; Sequence 230, Application US/10474794
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; Publication No. US20040213793A1
; GENERAL INFORMATION:
; APPLICANT: Carson-Walter, Eleanor
; APPLICANT: St. Croix, Brad
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00179
; CURRENT APPLICATION NUMBER: US/10/474,794
; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 60/308,829
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 359
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 230
; LENGTH: 500
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-474-794-230

Query Match      100.0%; Score 588; DB 17; Length 500;
Best Local Similarity 100.0%; Pred. No. 3.5e-60;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LSPDFPPYGHPLRQITTIATGCFIFMGDVHHRMLTATQYVAPLMAFNFGYSDNSTVYVFD 60
    |||||
Db 137 LSPDFPPYGHPLRQITTIATGCFIFMGDVHHRMLTATQYVAPLMAFNFGYSDNSTVYVFD 196
    |||||

Qy 61 NGTVFVQWHDVYVQWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPE 108
    |||||
Db 197 NGTVFVQWHDVYVQWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPE 244
    |||||

RESULT 8
US-10-357-819-2
; Sequence 2, Application US/10357819
; Publication No. US20040259774A1
; GENERAL INFORMATION:
; APPLICANT: Alvarez, Enrique
; APPLICANT: Edinger, Shomit R.
; APPLICANT: Gangolli, Esna A.
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Gorman, Linda
; APPLICANT: Guo, Xiaojia
; APPLICANT: Ji, Weizhen
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Li, Li
; APPLICANT: Miller, Charles E.
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Rastelli, Luca
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Svytek, Kimberly A.
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-538A
; CURRENT APPLICATION NUMBER: US/10/357,819
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 09/584,411
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 09/783,436
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 10/085,198
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 60/353,301
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 60/355,099
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; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: 60/356,424
; PRIOR FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: 60/358,239
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: 60/358,608
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/359,367
; PRIOR FILING DATE: 2002-02-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: Curaseq1ist version 0.1
; SEQ ID NO 2
; LENGTH: 500
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-357-819-2

Query Match      100.0%; Score 588; DB 17; Length 500;
Best Local Similarity 100.0%; Pred. No. 3.5e-60;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  LSPDFPFVGHPLRQITTAGTGFIWGDVVIHRMLTATQVAPLMAFNPGYSDNSTVVYFD 60
Db      137 LSFDPFPYVGHPLRQITTAGTGFIWGDVVIHRMLTATQVAPLMAFNPGYSDNSTVVYFD 196

Qy      61  NGTVFVQVQDHYVLQGWEDKGSFTFOAALHHDGGRIVFAYKEIPMSVPE 108
Db      197 NGTVFVQVQDHYVLQGWEDKGSFTFOAALHHDGGRIVFAYKEIPMSVPE 244

RESULT 9
US-10-156-487A-5
; Sequence 5, Application US/10156487A
; Publication No. US20030092025A1
; GENERAL INFORMATION:
; APPLICANT: Juan, Todd
; APPLICANT: Bass, Michael B.
; APPLICANT: Oliner, John
; TITLE OF INVENTION: Tumor Endothelial Marker 7a Molecules and Uses Thereof
; FILE REFERENCE: 01-072-A
; CURRENT APPLICATION NUMBER: US/10/156,487A
; CURRENT FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: 60/293,852
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-156-487A-5

Query Match      100.0%; Score 588; DB 14; Length 502;
Best Local Similarity 100.0%; Pred. No. 3.6e-60;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  LSPDFPFVGHPLRQITTAGTGFIWGDVVIHRMLTATQVAPLMAFNPGYSDNSTVVYFD 60
Db      137 LSFDPFPYVGHPLRQITTAGTGFIWGDVVIHRMLTATQVAPLMAFNPGYSDNSTVVYFD 196

Qy      61  NGTVFVQVQDHYVLQGWEDKGSFTFOAALHHDGGRIVFAYKEIPMSVPE 108
Db      197 NGTVFVQVQDHYVLQGWEDKGSFTFOAALHHDGGRIVFAYKEIPMSVPE 244

RESULT 10
US-09-918-715-179
; Sequence 179, Application US/09918715
; Publication No. US20030017157A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein

```

Publication No. US20030017157A1  
GENERAL INFORMATION:  
APPLICANT: Brad St. Croix  
APPLICANT: Bert Vogelstein  
APPLICANT: Kenneth Kinzler  
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS  
FILE REFERENCE: 1107.00134  
CURRENT APPLICATION NUMBER: US/09/918.715  
CURRENT FILING DATE: 2001-08-01  
PRIOR APPLICATION NUMBER: 60/222,599  
PRIOR FILING DATE: 2000-08-02  
PRIOR APPLICATION NUMBER: 60/224,360  
PRIOR FILING DATE: 2000-08-11  
PRIOR APPLICATION NUMBER: 60/282,850  
PRIOR FILING DATE: 2000-04-11  
NUMBER OF SEQ ID NOS: 358  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 192  
LENGTH: 500  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-918-715-192

Query Match 89.8%; Score 528; DB 10; Length 500;  
Best Local Similarity 91.5%; Pred. No. 3.9e-53;  
Matches 97; Conservative 4; Mismatches 5; Indels 0; Gaps 0;  
Qy 1 LSFDPFPGHPLRQITTIATGGFIFMGDVIHRMLTATQVAPLMANFNPGYSDNSTVYFD 60  
Db 138 LSFDPFPGHPLRQITTIATGGFIFMGDMLHRLMTATQVAPLMANFNPGYSDNSTVYFD 197  
Qy 61 NGTVFVQWDHVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPMSV 106  
Db 198 NGTVFVQWDHVYLQDREDRGSFTFQAALHHDGRIVFGYKEIPMAV 243

RESULT 13  
US-09-918-715-297  
Sequence 297, Application US/09918715  
Publication No. US20030017157A1  
GENERAL INFORMATION:  
APPLICANT: Brad St. Croix  
APPLICANT: Bert Vogelstein  
APPLICANT: Kenneth Kinzler  
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS  
FILE REFERENCE: 1107.00134  
CURRENT APPLICATION NUMBER: US/09/918.715  
CURRENT FILING DATE: 2001-08-01  
PRIOR APPLICATION NUMBER: 60/222,599  
PRIOR FILING DATE: 2000-08-02  
PRIOR APPLICATION NUMBER: 60/224,360  
PRIOR FILING DATE: 2000-08-11  
PRIOR APPLICATION NUMBER: 60/282,850  
PRIOR FILING DATE: 2000-04-11  
NUMBER OF SEQ ID NOS: 358  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 297  
LENGTH: 500  
TYPE: PRT  
ORGANISM: Mouse  
US-09-918-715-297

Query Match 89.8%; Score 528; DB 10; Length 500;  
Best Local Similarity 91.5%; Pred. No. 3.9e-53;  
Matches 97; Conservative 4; Mismatches 5; Indels 0; Gaps 0;  
Qy 1 LSFDPFPGHPLRQITTIATGGFIFMGDVIHRMLTATQVAPLMANFNPGYSDNSTVYFD 60  
Db 138 LSFDPFPGHPLRQITTIATGGFIFMGDMLHRLMTATQVAPLMANFNPGYSDNSTVYFD 197  
Qy 61 NGTVFVQWDHVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPMSV 106  
Db 198 NGTVFVQWDHVYLQDREDRGSFTFQAALHHDGRIVFGYKEIPMAV 243

## RESULT 14

US-10-156-487A-6  
Sequence 6, Application US/10156487A  
Publication No. US20030092025A1  
GENERAL INFORMATION:  
APPLICANT: Juan, Todd  
APPLICANT: Bass, Michael B.  
APPLICANT: Oliner, John  
TITLE OF INVENTION: Tumor Endothelial Marker 7a Molecules and Uses Thereof  
FILE REFERENCE: 01-072-A  
CURRENT APPLICATION NUMBER: US/10/156.487A  
CURRENT FILING DATE: 2002-09-10  
PRIOR APPLICATION NUMBER: 60/293,852  
PRIOR FILING DATE: 2001-05-25  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 6  
LENGTH: 500  
TYPE: PRT  
ORGANISM: Mus musculus  
US-10-156-487A-6

Query Match 89.8%; Score 528; DB 14; Length 500;  
Best Local Similarity 91.5%; Pred. No. 3.9e-53;  
Matches 97; Conservative 4; Mismatches 5; Indels 0; Gaps 0;  
Qy 1 LSFDPFPGHPLRQITTIATGGFIFMGDVIHRMLTATQVAPLMANFNPGYSDNSTVYFD 60  
Db 138 LSFDPFPGHPLRQITTIATGGFIFMGDMLHRLMTATQVAPLMANFNPGYSDNSTVYFD 197  
Qy 61 NGTVFVQWDHVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPMSV 106  
Db 198 NGTVFVQWDHVYLQDREDRGSFTFQAALHHDGRIVFGYKEIPMAV 243

## RESULT 15

US-10-474-794-192  
Sequence 192, Application US/10474794  
Publication No. US20040213793A1  
GENERAL INFORMATION:  
APPLICANT: Carson-Walter, Eleanor  
APPLICANT: St. Croix, Brad  
APPLICANT: Vogelstein, Bert  
APPLICANT: Kinzler, Kenneth  
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS  
FILE REFERENCE: 1107.00179  
CURRENT APPLICATION NUMBER: US/10/474.794  
CURRENT FILING DATE: 2003-10-14  
PRIOR APPLICATION NUMBER: 60/282,850  
PRIOR FILING DATE: 2001-04-11  
PRIOR APPLICATION NUMBER: 60/308,829  
PRIOR FILING DATE: 2001-08-01  
NUMBER OF SEQ ID NOS: 359  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 192  
LENGTH: 500  
TYPE: PRT  
ORGANISM: Mus musculus  
US-10-474-794-192

Query Match 89.8%; Score 528; DB 17; Length 500;  
Best Local Similarity 91.5%; Pred. No. 3.9e-53;  
Matches 97; Conservative 4; Mismatches 5; Indels 0; Gaps 0;  
Qy 1 LSFDPFPGHPLRQITTIATGGFIFMGDVIHRMLTATQVAPLMANFNPGYSDNSTVYFD 60  
Db 138 LSFDPFPGHPLRQITTIATGGFIFMGDMLHRLMTATQVAPLMANFNPGYSDNSTVYFD 197  
Qy 61 NGTVFVQWDHVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPMSV 106  
Db 198 NGTVFVQWDHVYLQDREDRGSFTFQAALHHDGRIVFGYKEIPMAV 243

Search completed: January 28, 2005, 22:19:18  
Job time : 33.518 secs

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OM protein - protein search, using sw model

Run on: January 28, 2005, 21:56:43 ; Search time 8.77562 Seconds  
(without alignments)  
816.164 Million cell updates/sec

Title: US-09-918-715-230\_COPY\_137\_244

Perfect score: 588

Sequence: 1 LSFDFPYGHLRQITATG.....LHHDGRIVFAYKEIPMSVPE 108

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.\*

- 1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/iaa/PTCUS\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	588	100.0	431	4	US-09-912-935-36
2	417	70.9	392	4	US-09-764-325A-23
3	417	70.9	392	4	US-09-764-325A-25
4	417	70.9	392	4	US-09-912-935-23
5	417	70.9	392	4	US-09-912-935-25
6	417	70.9	425	4	US-09-912-935-35
7	417	70.9	449	4	US-09-912-935-34
8	417	70.9	499	4	US-09-912-935-31
9	417	70.9	529	4	US-09-912-935-28
10	417	70.9	529	4	US-09-912-935-40
11	411	69.9	530	4	US-09-912-935-38
12	68	11.6	324	1	US-08-746-797-2
13	68	11.6	324	1	US-08-927-387-2
14	68	11.6	324	2	US-08-918-058-2
15	67	11.4	254	4	US-09-543-681A-7887
16	67	11.4	613	4	US-09-252-991A-19955
17	66	11.2	410	4	US-09-540-236-3584
18	66	11.2	454	4	US-09-450-209-16
19	66	11.2	738	3	US-08-989-385-1
20	66	11.2	738	4	US-09-593-826-1
21	65.5	11.1	262	4	US-09-543-681A-4675
22	64	10.9	363	3	US-09-195-666A-4
23	64	10.9	363	3	US-09-635-705-4
24	64	10.9	363	4	US-09-634-858A-4
25	64	10.9	363	4	US-08-869-927C-4
26	64	10.9	424	6	5169835-6
27	64	10.9	450	4	US-09-270-767-46295

28	64	10.9	565	3	US-09-008-481A-6	Sequence 6, Appli
29	64	10.9	565	3	US-09-195-666A-5	Sequence 5, Appli
30	64	10.9	565	3	US-09-195-666A-49	Sequence 49, Appli
31	64	10.9	565	3	US-09-309-592-6	Sequence 6, Appli
32	64	10.9	565	3	US-09-635-705-5	Sequence 5, Appli
33	64	10.9	565	3	US-09-635-705-49	Sequence 49, Appli
34	64	10.9	565	4	US-09-634-858A-5	Sequence 5, Appli
35	64	10.9	565	4	US-09-634-858A-49	Sequence 49, Appli
36	64	10.9	565	4	US-08-869-927C-5	Sequence 49, Appli
37	64	10.9	565	4	US-08-869-927C-49	Sequence 49, Appli
38	64	10.9	609	4	US-09-257-525A-9	Sequence 9, Appli
39	63.5	10.8	78	3	US-09-011-540-6	Sequence 6, Appli
40	63.5	10.8	377	2	US-08-929-922B-2	Sequence 2, Appli
41	63.5	10.8	377	3	US-09-342-394-2	Sequence 2, Appli
42	63.5	10.8	377	3	US-09-580-064-2	Sequence 2, Appli
43	63.5	10.8	377	3	US-09-011-540-2	Sequence 2, Appli
44	63.5	10.8	377	4	US-09-718-709-2	Sequence 2, Appli
45	63	10.7	220	4	US-09-583-110-2877	Sequence 2877, Ap

ALIGNMENTS

RESULT 1  
US-09-912-935-36  
; Sequence 36, Application US/09912935  
; Patent No. 6673904  
; GENERAL INFORMATION:  
; APPLICANT: Nishikawa, Mitsuo et al.  
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE POLYPEPTIDES AND POLYNUCLEOTIDES  
; FILE REFERENCE: 32066/37483  
; CURRENT APPLICATION NUMBER: US/09/912,935  
; CURRENT FILING DATE: 2001-07-24  
; PRIOR APPLICATION NUMBER: PCT/US00/35260  
; PRIOR FILING DATE: 2000-12-23  
; NUMBER OF SEQ ID NOS: 53  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 36  
; LENGTH: 431  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-912-935-36

Query Match	100.0%;	Score 588;	DB 4;	Length 431;
Best Local Similarity	100.0%;	Pred. No. 2e-66;		
Matches	108;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
Qy	1	LSFDFPYGHLRQITATGTFPMGDVHRMLTATQVAPLMAFNFGYSDNSTVYVFD	60	
Db	66	LSFDFPYGHLRQITATGTFPMGDVHRMLTATQVAPLMAFNFGYSDNSTVYVFD	125	
Qy	61	NGTVFVQWDRHYVLOGWEDKGSFTFOALHHDGRIVFAYKEIPMSVPE	108	
Db	126	NGTVFVQWDRHYVLOGWEDKGSFTFOALHHDGRIVFAYKEIPMSVPE	173	

RESULT 2  
US-09-764-325A-23  
; Sequence 23, Application US/09764325A  
; Patent No. 6667391  
; GENERAL INFORMATION:  
; APPLICANT: Labat, Ivan  
; APPLICANT: Drmanac, Radoje T.  
; APPLICANT: Tang, Y. T.  
; APPLICANT: Chao, Cheng-Chi  
; APPLICANT: Childs, John  
; APPLICANT: Methods and Materials Relating to No. 6667391el Stem Cell  
; TITLE OF INVENTION: Growth Factor-Like Polypeptides and Polynucleotides  
; FILE REFERENCE: 30266/37630A  
; CURRENT APPLICATION NUMBER: US/09/764,325A  
; CURRENT FILING DATE: 2001-01-16



FILE REFERENCE: 32066/37483  
CURRENT APPLICATION NUMBER: US/09/912,935  
CURRENT FILING DATE: 2001-07-24  
PRIOR APPLICATION NUMBER: PCT/US00/35260  
PRIOR FILING DATE: 2000-12-23  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 35  
LENGTH: 425  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-912-935-35

Query Match 70.9%; Score 417; DB 4; Length 425;  
Best Local Similarity 72.2%; Pred. No. 1.2e-44;  
Matches 78; Conservative 12; Mismatches 18; Indels 0; Gaps 0;  
QY 1 LSFDPFPGHPLRQITATGGFIFMGDVHRLMTATQVAPLMANFNPGYSDNSTVYVD 60  
DB 59 LSFDPFPGHFLREITATGGFIYTGVEVHRMLTATQIAPLMANFDFSVSRNSTVRYFD 118  
QY 61 NGTVFVQWDHVYLGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPE 108  
DB 119 NGTALVQWDHVHLQDYNLGSFTFQATLLMDGRIFGYKEIPVLVTQ 166

RESULT 7  
US-09-912-935-34  
Sequence 34, Application US/09912935  
Patent No. 6673904  
GENERAL INFORMATION:  
APPLICANT: Nishikawa, Mitsuo et al.  
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE  
FILE REFERENCE: 32066/37483  
CURRENT APPLICATION NUMBER: US/09/912,935  
CURRENT FILING DATE: 2001-07-24  
PRIOR APPLICATION NUMBER: PCT/US00/35260  
PRIOR FILING DATE: 2000-12-23  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 34  
LENGTH: 449  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-912-935-34

Query Match 70.9%; Score 417; DB 4; Length 449;  
Best Local Similarity 72.2%; Pred. No. 1.3e-44;  
Matches 78; Conservative 12; Mismatches 18; Indels 0; Gaps 0;  
QY 1 LSFDPFPGHPLRQITATGGFIFMGDVHRLMTATQVAPLMANFNPGYSDNSTVYVD 60  
DB 161 LSFDPFPGHFLREITATGGFIYTGVEVHRMLTATQIAPLMANFDFSVSRNSTVRYFD 220  
QY 61 NGTVFVQWDHVYLGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPE 108  
DB 221 NGTALVQWDHVHLQDYNLGSFTFQATLLMDGRIFGYKEIPVLVTQ 268

RESULT 8  
US-09-912-935-31  
Sequence 31, Application US/09912935  
Patent No. 6673904  
GENERAL INFORMATION:  
APPLICANT: Nishikawa, Mitsuo et al.  
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE  
FILE REFERENCE: 32066/37483  
CURRENT APPLICATION NUMBER: US/09/912,935  
CURRENT FILING DATE: 2001-07-24  
PRIOR APPLICATION NUMBER: PCT/US00/35260  
PRIOR FILING DATE: 2000-12-23

NUMBER OF SEQ ID NOS: 53  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 31  
LENGTH: 499  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-912-935-31

Query Match 70.9%; Score 417; DB 4; Length 499;  
Best Local Similarity 72.2%; Pred. No. 1.5e-44;  
Matches 78; Conservative 12; Mismatches 18; Indels 0; Gaps 0;  
QY 1 LSFDPFPGHPLRQITATGGFIFMGDVHRLMTATQVAPLMANFNPGYSDNSTVYVD 60  
DB 131 LSFDPFPGHFLREITATGGFIYTGVEVHRMLTATQIAPLMANFDFSVSRNSTVRYFD 190  
QY 61 NGTVFVQWDHVYLGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPE 108  
DB 191 NGTALVQWDHVHLQDYNLGSFTFQATLLMDGRIFGYKEIPVLVTQ 238

RESULT 9  
US-09-912-935-28  
Sequence 28, Application US/09912935  
Patent No. 6673904  
GENERAL INFORMATION:  
APPLICANT: Nishikawa, Mitsuo et al.  
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE  
FILE REFERENCE: 32066/37483  
CURRENT APPLICATION NUMBER: US/09/912,935  
CURRENT FILING DATE: 2001-07-24  
PRIOR APPLICATION NUMBER: PCT/US00/35260  
PRIOR FILING DATE: 2000-12-23  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 28  
LENGTH: 529  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-912-935-28

Query Match 70.9%; Score 417; DB 4; Length 529;  
Best Local Similarity 72.2%; Pred. No. 1.6e-44;  
Matches 78; Conservative 12; Mismatches 18; Indels 0; Gaps 0;  
QY 1 LSFDPFPGHPLRQITATGGFIFMGDVHRLMTATQVAPLMANFNPGYSDNSTVYVD 60  
DB 161 LSFDPFPGHFLREITATGGFIYTGVEVHRMLTATQIAPLMANFDFSVSRNSTVRYFD 220  
QY 61 NGTVFVQWDHVYLGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPE 108  
DB 221 NGTALVQWDHVHLQDYNLGSFTFQATLLMDGRIFGYKEIPVLVTQ 268

RESULT 10  
US-09-912-935-40  
Sequence 40, Application US/09912935  
Patent No. 6673904  
GENERAL INFORMATION:  
APPLICANT: Nishikawa, Mitsuo et al.  
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE  
FILE REFERENCE: 32066/37483  
CURRENT APPLICATION NUMBER: US/09/912,935  
CURRENT FILING DATE: 2001-07-24  
PRIOR APPLICATION NUMBER: PCT/US00/35260  
PRIOR FILING DATE: 2000-12-23  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 40  
LENGTH: 529  
TYPE: PRT

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; ORGANISM: Homo sapiens
US-09-912-935-40

Query Match      70.9%; Score 417; DB 4; Length 529;
Best Local Similarity 72.2%; Pred. No. 1.6e-44;
Matches 78; Conservative 12; Mismatches 18; Indels 0; Gaps 0;

Qy 1 LSFDPFFYGHPLRQITTIATGGFIFMGDVHRLMTATQVAPLMANFNFGYSDNSTVVYFD 60
Db 161 LSFDPFFYGHFLREITVATGGFIYTGVEVVRHRLMTATQVAPLMANFDSVSRNSTVRYFD 220

Qy 61 NGTVFVQWQDVHVLQGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPE 108
Db 221 NGTALVQWQDVHVLQDNYNLGSFTFQAATLLMDGRIIFGYKEIPVLVTQ 268

RESULT 11
US-09-912-935-38
; Sequence 38, Application US/09912935
; Patent No. 6673904
; GENERAL INFORMATION:
; APPLICANT: Nishikawa, Mitsu et al.
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
; FILE REFERENCE: 32066/37483
; CURRENT APPLICATION NUMBER: US/09/912,935
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: PCT/US00/35260
; PRIOR FILING DATE: 2000-12-23
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 38
; LENGTH: 530
; TYPE: PRT
; ORGANISM: Mouse
US-09-912-935-38

Query Match      69.9%; Score 411; DB 4; Length 530;
Best Local Similarity 70.4%; Pred. No. 9.5e-44;
Matches 76; Conservative 13; Mismatches 19; Indels 0; Gaps 0;

Qy 1 LSFDPFFYGHPLRQITTIATGGFIFMGDVHRLMTATQVAPLMANFNFGYSDNSTVVYFD 60
Db 161 LSFDPFFYGHFLNEVTATGGFIYTGVEVVRHRLMTATQVAPLMANFDSVSRNSTVRYFD 220

Qy 61 NGTVFVQWQDVHVLQGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPE 108
Db 221 NGTALVQWQDVHVLQDNYNLGSFTFQAATLLMDGRIIFGYKEIPVLVTQ 268

RESULT 12
US-08-746-797-2
; Sequence 2, Application US/08746797
; Patent No. 5759832
; GENERAL INFORMATION:
; APPLICANT: Gentry, Daniel
; APPLICANT: Lonsdale, John
; APPLICANT: Payne, David
; APPLICANT: Pearson, Stewart
; TITLE OF INVENTION: NOVEL FabH
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/746,797
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: No. 5759832 Yet Assigned
; FILING DATE: 23-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimmi, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P50573
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 324 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; US-08-746-797-2

Query Match      11.6%; Score 68; DB 1; Length 324;
Best Local Similarity 23.5%; Pred. No. 2.6;
Matches 31; Conservative 19; Mismatches 36; Indels 46; Gaps 7;

Qy 15 ITIATGGFIFMGDVHRLMTATQVAPLMANFNFG-----YSDNSTVVYFDN 61
Db 108 LTAACSGFVF-----ALSTAEEKFIA--SGRFQKGLVIGSETLSKAVDWSDRSTAVLFGD 159

Qy 62 GTVPVW-----QWDHVYLQGWEDKGS-----FTFQAA-----LHHDGRIV-- 96
Db 160 GAGGVLLAESEQEHFLAESLNSDGRSECLTYGHSLGSLSPFSDQESADSLFKMDGRITVFD 219

Qy 97 FAYKEIPMSVPE 108
Db 220 FAIRDVAKSIQK 231

RESULT 13
US-08-927-387-2
; Sequence 2, Application US/08927387
; Patent No. 5783432
; GENERAL INFORMATION:
; APPLICANT: Gentry, Daniel
; APPLICANT: Lonsdale, John
; APPLICANT: Payne, David
; APPLICANT: Pearson, Stewart
; TITLE OF INVENTION: NOVEL FabH
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/927,387
; FILING DATE: 25-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
```

APPLICATION NUMBER: 08/746,797  
FILING DATE: 23-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Gimmi, Edward R  
REGISTRATION NUMBER: 38,891  
REFERENCE/DOCKET NUMBER: P50573  
TELEPHONE: 610-270-4478  
TELEFAX: 610-270-5090  
TELEX:  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 324 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
US-08-927-387-2

Query Match 11.6%; Score 68; DB 1; Length 324;  
Best Local Similarity 23.5%; Pred. No. 2.6;  
Matches 31; Conservative 19; Mismatches 36; Indels 46; Gaps 7;  
QY 15 ITIATGGFIEMGDVIHRMLTATQYVAPLMAFNFG-----YSDNSTVWYFDN 61  
DB 108 LTACSGFV-----ALSTAEKFA--SGRFQGLVIGSTLSKAVDWSRSTAVLFGD 159  
QY 62 GTVFV-----QWDHVYLQGWEDKGS-----FTFQAA-----LHHDGRIV-- 96  
DB 160 GAGGVILLEASQEHFLAESLNSDGRSCLTYGHSLGHSFSDQESADSLFKMDGRTVFD 219  
QY 97 PAYKEIPMSVPE 108  
DB 220 FAIRDVAKSINQ 231

RESULT 14  
US-08-918-058-2  
Sequence 2, Application US/08918058  
Patent No. 5885572  
GENERAL INFORMATION:  
APPLICANT: Gentry, Daniel  
APPLICANT: Lonsdale, John  
APPLICANT: Payne, David  
APPLICANT: Pearson, Stewart  
TITLE OF INVENTION: NOVEL FABH  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corporation  
STREET: 709 Swedeland Road  
CITY: King of Prussia  
STATE: PA  
COUNTRY: U.S.A.  
ZIP: 19406-0939  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/918,058  
FILING DATE: 25-AUG-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/746,797  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Gimmi, Edward R  
REGISTRATION NUMBER: 38,891

REFERENCE/DOCKET NUMBER: P50573  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-270-4478  
TELEFAX: 610-270-5090  
TELEX:  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 324 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
US-08-918-058-2

Query Match 11.6%; Score 68; DB 2; Length 324;  
Best Local Similarity 23.5%; Pred. No. 2.6;  
Matches 31; Conservative 19; Mismatches 36; Indels 46; Gaps 7;  
QY 15 ITIATGGFIEMGDVIHRMLTATQYVAPLMAFNFG-----YSDNSTVWYFDN 61  
DB 108 LTACSGFV-----ALSTAEKFA--SGRFQGLVIGSTLSKAVDWSRSTAVLFGD 159  
QY 62 GTVFV-----QWDHVYLQGWEDKGS-----FTFQAA-----LHHDGRIV-- 96  
DB 160 GAGGVILLEASQEHFLAESLNSDGRSCLTYGHSLGHSFSDQESADSLFKMDGRTVFD 219  
QY 97 PAYKEIPMSVPE 108  
DB 220 FAIRDVAKSINQ 231

RESULT 15  
US-09-543-681A-7887  
Sequence 7887, Application US/09543681A  
Patent No. 6605709  
GENERAL INFORMATION:  
APPLICANT: GARY BRETON  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS  
FILE REFERENCE: 2709.1002-001  
CURRENT APPLICATION NUMBER: US/09/543,681A  
CURRENT FILING DATE: 2000-04-05  
PRIOR APPLICATION NUMBER: US 60/128,706  
PRIOR FILING DATE: 1999-04-09  
NUMBER OF SEQ ID NOS: 8344  
SEQ ID NO 7887  
LENGTH: 254  
TYPE: PRT  
ORGANISM: Proteus mirabilis  
US-09-543-681A-7887

Query Match 11.4%; Score 67; DB 4; Length 254;  
Best Local Similarity 26.5%; Pred. No. 2.5;  
Matches 22; Conservative 15; Mismatches 30; Indels 16; Gaps 3;  
QY 16 TIATGGFIEMGDVIHRMLTATQYVAPL--MANFNPGYSDNSTVWYFDNGTVFVQ----- 68  
DB 135 SIKTGGILIGEPYWRQIPTTQETIAQACGASSISDFLTLSLVSFDFNQGYDLVEMVLAD 194  
QY 69 ---WDH-----VYLGWEDKGS 82  
DB 195 QEGWDRYEAKWMTTMRRLDKNS 217

Search completed: January 28, 2005, 22:14:13  
Job time : 10.0256 secs

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Result No.	Score	Query			ID	Description
		Match	Length	DB		
1	588	100.0	351	2	Q6ZSC8	Q6zac8 homo sapien
2	588	100.0	351	2	BAC87025	BAC87025 homo sapi
3	588	100.0	500	2	Q9HCT9	Q9hct9 homo sapien
4	585	99.5	500	2	Q8UKV5	Q8luk5 homo sapien
5	528	89.8	500	2	Q9CWW5	Q9cww5 mus musculu
6	528	89.8	500	2	Q81ZV7	Q81zv7 mus musculu
7	528	89.8	507	2	Q8BM20	Q8bm20 mus musculu
8	417	70.9	480	2	Q9GE59	Q9ge59 homo sapien
9	417	70.9	529	2	Q6UX71	Q6ux71 homo sapien
10	417	70.9	529	2	Q9GPD9	Q9gpd9 homo sapien
11	417	70.9	529	2	AAQ88850	AAQ88850 homo sapi
12	413	70.2	513	2	Q6DE92	Q6de92 xenopus lae
13	411	69.9	530	2	Q6PBT5	Q6pet5 mus musculu
14	411	69.9	530	2	Q9DC11	Q9dc11 mus musculu
15	411	69.9	530	2	Q91ZV6	Q91zv6 mus musculu
16	411	69.9	530	2	AAH57881	AAH57881 mus muscu
17	317.5	54.0	498	2	Q1B500	Q1B500 caenorhabdi
18	304	51.7	625	2	Q9W2V9	Q9w2v9 drosophila
19	249	42.3	77	2	Q7RJF7	Q7rjf7 anopheles g
20	220.5	37.5	274	2	Q7R3F6	Q7r3f6 anopheles g
21	210.5	35.8	384	2	Q7Q2J8	Q7q2j8 anopheles g
22	123	20.9	1161	2	Q04901	Q04901 halocynthia
23	87.5	14.9	1324	2	Q7YZ28	Q7yz28 cryptospori
24	86	14.6	1538	2	Q7PFF6	Q7pff6 anopheles g
25	86	14.6	2223	2	Q7Q1V0	Q7q1v0 anopheles g
26	84.5	14.4	315	2	Q6URR8	Q6urr8 xenopus lae
27	84.5	14.4	315	2	AAQ62573	AAQ62573 xenopus l
28	84	14.3	121	1	SHH_CARAU	P79691 carassius a
29	84	14.3	121	1	SHH_PUNCO	P79838 puntius con
30	84	14.3	121	1	SHH_PUNTE	P79850 puntius tet
31	84	14.3	121	1	SHH_RASEL	P79858 rasbora ele

```
RN
RP SEQUENCE FROM N.A.
RA Oshima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K.,
RA Arita M., Mueashino K., Yuuki H., Hara H., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Umezawa A., Imabayashi H.,
RA Fukuma M., Hata J., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y.,
RA Saito K., Nishikawa T., Kimura K., Yamashita H., Matsu K.,
RA Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagaatsuma M.,
RA Murakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y.,
RA Sugano S., Nagahari K., Maeuho Y., Nagai K., Isogai T.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK127539; BAC87025.1; -.
SQ SEQUENCE 351 AA; 39639 MW; FE03CC9D78E4604A CRC64;

Query Match 100.0%; Score 588; DB 2; Length 351;
Best Local Similarity 100.0%; Pred. No. 6.8e-54;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LSFDFPFYGHPLRQITTIATGGFIFMGDVHHRMLTATQYVAPLMANFNPGYSDNSTVVYFD 60
Db 130 LSFDFPFYGHPLRQITTIATGGFIFMGDVHHRMLTATQYVAPLMANFNPGYSDNSTVVYFD 189

Qy 61 NGTVFVQWQDHVYLGQWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPE 108
Db 190 NGTVFVQWQDHVYLGQWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPE 237

RESULT 3
Q9HCT9
ID Q9HCT9 PRELIMINARY; PRT; 500 AA.
AC Q9HCT9
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Tumor endothelial marker 7 precursor (Tumor endothelial marker 3
DE precursor).
GN Name=TEM7;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=20407466; PubMed=10947988;
RA St Croix B., Rago C., Velculescu V., Traverso G., Romans K.E.,
RA Montgomery E., Lai A., Riggins G.J., Lengauer C., Vogelstein B.,
RA Kinzler K.W.;
RT "Genes expressed in human tumor endothelium.";
RL Science 289:1197-1202(2000).
[2]
RN SEQUENCE FROM N.A.
RP St Croix B., Vogelstein B., Kinzler K.W.;
RA Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
[3]
RN SEQUENCE FROM N.A.
RP MEDLINE=21443268; PubMed=11559528;
RA Carson-Walter E.B., Watkins D.N., Nanda A., Vogelstein B.,
RA Kinzler K.W., St Croix B.;
RT "Cell surface tumor endothelial markers are conserved in mice and
RT humans.";
RL Cancer Res. 61:6649-6655(2001).
RL EMBL; AF279144; AAG00869.2; -.
DR EMBL; AF378753; AAL11990.1; -.
DR GO; GO:0001525; P:angiogenesis; NAS.
DR InterPro; IPR003659; Plexin-like.
DR InterPro; IPR002165; Plexin_repeat.
DR Pfam; PF01437; PSI; 1.
DR SMART; SM00423; PSI; 1.
KW Signal.
FT SIGNAL 1 18 Potential.
FT CHAIN 19 500 tumor endothelial marker 3.
SQ SEQUENCE 500 AA; 55760 MW; C545A16619EEDBED CRC64;
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RN
RP SEQUENCE FROM N.A.
RA Oshima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K.,
RA Arita M., Mueashino K., Yuuki H., Hara H., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Umezawa A., Imabayashi H.,
RA Fukuma M., Hata J., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y.,
RA Saito K., Nishikawa T., Kimura K., Yamashita H., Matsu K.,
RA Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagaatsuma M.,
RA Murakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y.,
RA Sugano S., Nagahari K., Maeuho Y., Nagai K., Isogai T.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK127539; BAC87025.1; -.
SQ SEQUENCE 351 AA; 39639 MW; FE03CC9D78E4604A CRC64;

Query Match 100.0%; Score 588; DB 2; Length 500;
Best Local Similarity 100.0%; Pred. No. 1e-53;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LSFDFPFYGHPLRQITTIATGGFIFMGDVHHRMLTATQYVAPLMANFNPGYSDNSTVVYFD 60
Db 137 LSFDFPFYGHPLRQITTIATGGFIFMGDVHHRMLTATQYVAPLMANFNPGYSDNSTVVYFD 196

Qy 61 NGTVFVQWQDHVYLGQWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPE 108
Db 197 NGTVFVQWQDHVYLGQWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPE 244

RESULT 4
Q8IUUK5
ID Q8IUUK5 PRELIMINARY; PRT; 500 AA.
AC Q8IUUK5
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Plexin domain containing 1,.
GN Name=PLXDC1;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RP TISSUE=Testis;
RC MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A.C., Shevchenko S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Gramwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marz M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN SEQUENCE FROM N.A.
RP TISSUE=Testis;
RC Strausberg R.;
RA Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC036059; AAH36059.1; -.
DR Genew; HGNC:20945; PLXDC1.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007275; P:development; IEA.
DR InterPro; IPR003659; Plexin-like.
DR InterPro; IPR002165; Plexin_repeat.
DR Pfam; PF01437; PSI; 1.
DR SMART; SM00423; PSI; 1.
SQ SEQUENCE 500 AA; 55778 MW; 3FA4F9D98A514ABF CRC64;

Query Match 99.5%; Score 585; DB 2; Length 500;
Best Local Similarity 99.1%; Pred. No. 2.1e-53;
Matches 107; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LSFDFPFYGHPLRQITTIATGGFIFMGDVHHRMLTATQYVAPLMANFNPGYSDNSTVVYFD 60
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Db 137 LSPDFPFYGHPLRQITATGCGFIPMGDVHHRMLTATQYVAPLMANFNPYSDNSTVVYFD 196
Qy 61 NGTVFVQWHDVYVQWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPE 108
    |||||
Db 197 NGTVFVQWHDVYVQWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPE 244
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RESULT 5
Q9CWF5 PRELIMINARY; PRT; 500 AA.
AC Q9CWF5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus ES cells cDNA, RIKEN full-length enriched library,
DE clone-2410003107 product:TUMOR ENDOTHELIAL MARKER 7 homolog.
GN Name=Flxcl1;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN PANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RL prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
[5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuami T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yanamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
[6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,

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RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Segabe Y., Suzuki H., Tagami M., Tagawa A., Takabaishi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RA Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL; AK010361; BAB26881.1; -.
DR MGD; MGI:1919574; Plxcl1.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007275; P:development; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003659; Plexin-like.
DR InterPro; IPR002165; Plexin_repeat.
DR Pfam; PF01437; PSI; 1.
DR SMART; SM00423; PSI; 1.
SQ SEQUENCE 500 AA; 55635 MW; 802D6865F8C1A18BD CRC64;

Query Match 89.8%; Score 528; DB 2; Length 500;
Best Local Similarity 91.5%; Pred. No. 2.4e-47;
Matches 97; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LSPDFPFYGHPLRQITATGCGFIPMGDVHHRMLTATQYVAPLMANFNPYSDNSTVVYFD 60
    |||||
Db 138 LSPDFPFYGHPLRQITATGCGFIPMGDVHHRMLTATQYVAPLMANFNPYSDNSTVVYFD 197
    |||||

Qy 61 NGTVFVQWHDVYVQWEDKGSFTFOAALHHDGRIVFAYKEIPMSV 106
    |||||
Db 198 NGTVFVQWHDVYVQWEDKGSFTFOAALHHDGRIVFAYKEIPMAV 243
    |||||

RESULT 6
Q91ZV7 PRELIMINARY; PRT; 500 AA.
AC Q91ZV7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Tumor endothelial marker 7 precursor.
GN Name=Plxcl1; Synonyms=Tem7;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21443268; PubMed=11559528;
RA Carson-Walter E.B., Watkins D.N., Nanda A., Vogelstein B.,
RA Kinzler K.W., St Croix B.;
RT "Cell surface tumor endothelial markers are conserved in mice and
RT humans.";
RL Cancer Res. 61:6649-6655(2001).
DR EMBL; AF378760; AAL11997.1; -.
DR MGD; MGI:1919574; Plxcl1.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007275; P:development; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003659; Plexin-like.
DR InterPro; IPR002165; Plexin_repeat.
DR Pfam; PF01437; PSI; 1.
DR SMART; SM00423; PSI; 1.
KW Signal.
FT SIGNAL
FT CHAIN
SQ SEQUENCE 500 AA; 55693 MW; 14FE25512A319DAF CRC64;

Query Match 89.8%; Score 528; DB 2; Length 500;
Best Local Similarity 91.5%; Pred. No. 2.4e-47;
Matches 97; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

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Qy 1 LSFDFPPYGHPLRQITATGGTGFPMGDVHRLMTATQVAPLMAFNPGYSDNSTVYVFD 60
Db 138 LSFDFPPYGHPLRQITATGGTGFPMGDVHRLMTATQVAPLMAFNPGYSDNSTVYVFD 197
Qy 61 NGTVFVQVQWHDVYLQWEDKGSFTFQAALHHDGRIVFYAYKEIPMSV 106
Db 198 NGTVFVQVQWHDVYLQWEDKGSFTFQAALHHDGRIVFYAYKEIPMAV 243

RESULT 7
Q8BM20
ID Q8BM20 PRELIMINARY; PRT; 507 AA.
AC Q8BM20;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 16 days neonate cerebellum cDNA, RIKEN full-length
DE enriched library, clone:9630040L07 product:TUMOR ENDOTHELIAL MARKER 7
DE homolog.
GN Name=Plxdc1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=21085660; PubMed=11217851;
RA The FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,

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RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayaehida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK036144; BAC29318.1; -.
DR MGD; MGI:1919574; Plxdc1.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007275; P:development; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003659; Plexin-like.
DR InterPro; IPR002165; Plexin_repeat.
DR Pfam; PF01437; PSI; 1.
DR SMART; SM00423; PSI; 1.
SQ SEQUENCE 507 AA; 56332 MW; C2D50B44561C3415 CRC64;

Query Match 89.8%; Score 528; DB 2; Length 507;
Best Local Similarity 91.5%; Pred. No. 2.4e-47;
Matches 97; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LSFDFPPYGHPLRQITATGGTGFPMGDVHRLMTATQVAPLMAFNPGYSDNSTVYVFD 60
Db 145 LSFDFPPYGHPLRQITATGGTGFPMGDVHRLMTATQVAPLMAFNPGYSDNSTVYVFD 204
Qy 61 NGTVFVQVQWHDVYLQWEDKGSFTFQAALHHDGRIVFYAYKEIPMSV 106
Db 205 NGTVFVQVQWHDVYLQWEDKGSFTFQAALHHDGRIVFYAYKEIPMAV 250

RESULT 8
ID Q96E59 PRELIMINARY; PRT; 480 AA.
AC Q96E59;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE PLXDC2 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=22386257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heiton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]

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RP SEQUENCE FROM N.A.
RC TISSUE-Ovary;
RA Strausberg R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC012885; AAH12885.1; -.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR GO: GO:0007275; P:development; IEA.
DR InterPro: IPR003659; Plexin-like.
DR InterPro: IPR002165; Plexin_repeat.
DR Pfam: PF01437; PSI: 1.
DR SMART: SM00423; PSI: 1.
DR SEQUENCE 480 AA; 53912 MW; F8DB0E2631BC7816 CRC64;

Query Match 70.9%; Score 417; DB 2; Length 480;
Best Local Similarity 72.2%; Pred. No. 1.5e-35;
Matches 78; Conservative 12; Mismatches 18; Indels 0; Gaps 0;

Qy 1 LSPDFPPYGHPLRQITATGTFIFMGDVHRLMTATQYVAPLMANFNGYSDNSTVYFD 60
Dy 112 LSPDFPPYGHPLRQITATGTFIFMGDVHRLMTATQYVAPLMANFNGYSDNSTVYFD 171
Qy 61 NGTVFVQWQDHVYLGWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPE 108
Dy 172 NGTALVQWQDHVYLGWEDKGSFTFOAALHHDGRIVFAYKEIPVLTQ 219

RESULT 9
Q6UX71 PRELIMINARY; PRT; 529 AA.
AC Q6UX71;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE ARPP2514.
GN ORFNames=UNQ2514;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wleand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
DR EMBL: AY358486; AAQ88850.1; -.
DR InterPro: IPR003659; Plexin-like.
DR InterPro: IPR002165; Plexin_repeat.
DR Pfam: PF01437; PSI: 1.
DR SMART: SM00423; PSI: 1.
DR SEQUENCE 529 AA; 59583 MW; CCE911D6DF837B40 CRC64;

Query Match 70.9%; Score 417; DB 2; Length 529;
Best Local Similarity 72.2%; Pred. No. 1.5e-35;
Matches 78; Conservative 12; Mismatches 18; Indels 0; Gaps 0;

Qy 1 LSPDFPPYGHPLRQITATGTFIFMGDVHRLMTATQYVAPLMANFNGYSDNSTVYFD 60
Dy 161 LSPDFPPYGHPLRQITATGTFIFMGDVHRLMTATQYVAPLMANFNGYSDNSTVYFD 220
Qy 61 NGTVFVQWQDHVYLGWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPE 108
Dy 112 LSPDFPPYGHPLRQITATGTFIFMGDVHRLMTATQYVAPLMANFNGYSDNSTVYFD 171
Qy 61 NGTVFVQWQDHVYLGWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPE 108
Dy 172 NGTALVQWQDHVYLGWEDKGSFTFOAALHHDGRIVFAYKEIPVLTQ 219

RESULT 10
Q96PD9 PRELIMINARY; PRT; 529 AA.
AC Q96PD9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Tumor endothelial marker 7-related precursor.
GN Name=TEM7R;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21443268; PubMed=11559528;
RA Carson-Walter E.B., Watkins D.N., Nanda A., Vogelstein B.,
RA Kinzler K.W., St Croix B.;
RT "Cell surface tumor endothelial markers are conserved in mice and
RT humans.";
RL Cancer Res. 61:6649-6655(2001).
DR EMBL: AF378757; AAL11994.1; -.
DR GenBank: HGNC:21013; PLXDC2.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0004872; P:receptor activity; IEA.
DR GO: GO:0007275; P:development; IEA.
DR InterPro: IPR003659; Plexin-like.
DR InterPro: IPR002165; Plexin_repeat.
DR Pfam: PF01437; PSI: 1.
DR SMART: SM00423; PSI: 1.
DR Signal.
FT SIGNAL 1 30 Potential.
FT CHAIN 31 529 tumor endothelial marker 7-related.
SQ SEQUENCE 529 AA; 59583 MW; D44A0975DF894840 CRC64;

Query Match 70.9%; Score 417; DB 2; Length 529;
Best Local Similarity 72.2%; Pred. No. 1.5e-35;
Matches 78; Conservative 12; Mismatches 18; Indels 0; Gaps 0;

Qy 1 LSPDFPPYGHPLRQITATGTFIFMGDVHRLMTATQYVAPLMANFNGYSDNSTVYFD 60
Dy 161 LSPDFPPYGHPLRQITATGTFIFMGDVHRLMTATQYVAPLMANFNGYSDNSTVYFD 220
Qy 61 NGTVFVQWQDHVYLGWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPE 108
Dy 221 NGTALVQWQDHVYLGWEDKGSFTFOAALHHDGRIVFAYKEIPVLTQ 268

RESULT 11
AAQ88850 PRELIMINARY; PRT; 529 AA.
AC AAQ88850;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE ARPP2514.
GN UNQ2514.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12975309;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,

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Db 161 LSPDFPPYGHFLNEVTATGGFIYTGVEVHRLTATQYIAPLMAFPDPSVSRNSTVRYFD 220
Qy 61 NGTVFVQWDRHYVLQWEDKGSFTFOALHHDGRIVFAYKEIPMSVPE 108
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 221 NGTALVVQWDRHYVHLQDNYNLGSFTFOATLLMDGRIFGYKEIPVLVTQ 268

RESULT 14
Q9DC11 PRELIMINARY; PRT; 530 AA.
AC Q9DC11;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus adult male lung cDNA, RIKEN full-length enriched library,
DE clone:1200007L24 product:TUMOR ENDOTHELIAL MARKER 7-RELATED
DE homolog.
GN Name=Plxdc2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu M., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,

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RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK004640; BAB23431.1; -
DR MGD; MGI:1914698; Plxdc2.
DR GO; GO:0016020; C-membrane; IEA.
DR GO; GO:0004872; P:receptor activity; IEA.
DR GO; GO:0007275; P:development; IEA.
DR InterPro; IPR008947; PLCNuclease.
DR InterPro; IPR003659; Plexin-like.
DR InterPro; IPR002165; plexin_repeat.
DR Pfam; PF01437; PSI; 1.
DR SMART; SM00423; PSI; 1.
SQ SEQUENCE 530 AA; 59616 MW; FB956C020735E36D CRC64;

Query Match 69.9%; Score 411; DB 2; Length 530;
Best Local Similarity 70.4%; Pred. No. 6.4e-35;
Matches 76; Conservative 13; Mismatches 19; Indels 0; Gaps 0;

Qy 1 LSPDFPPYGHFLRQITATGGFIYTGVEVHRLTATQYIAPLMAFPDPSVSRNSTVRYFD 60
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Db 161 LSPDFPPYGHFLNEVTATGGFIYTGVEVHRLTATQYIAPLMAFPDPSVSRNSTVRYFD 220

Qy 61 NGTVFVQWDRHYVLQWEDKGSFTFOALHHDGRIVFAYKEIPMSVPE 108
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 221 NGTALVVQWDRHYVHLQDNYNLGSFTFOATLLMDGRIFGYKEIPVLVTQ 268

RESULT 15
Q91ZV6 PRELIMINARY; PRT; 530 AA.
AC Q91ZV6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Tumor endothelial marker 7-related precursor.
GN Name=Plxdc2; Synonyms=fem7R;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21443268; PubMed=11559528;
RA Carson-Walter E.B., Watkins D.N., Nanda A., Vogelstein B.,
RA Kinzler K.W., St Croix B.;
RT "Cell surface tumor endothelial markers are conserved in mice and
RT humans.";
RL Cancer Res. 61:6649-6655(2001).
DR EMBL; AF378761; AAL1998.1; -
DR MGD; MGI:1914698; Plxdc2.
DR GO; GO:0016020; C-membrane; IEA.
DR GO; GO:0004872; P:receptor activity; IEA.
DR GO; GO:0007275; P:development; IEA.
DR InterPro; IPR003659; Plexin-like.
DR InterPro; IPR002165; plexin_repeat.
DR Pfam; PF01437; PSI; 1.
DR SMART; SM00423; PSI; 1.
KW Signal.
FT SIGNAL 1 30 Potential.
FT CHAIN 31 530 tumor endothelial marker 7-related.
SQ SEQUENCE 530 AA; 59625 MW; FF8315020735E36D CRC64;

Query Match 69.9%; Score 411; DB 2; Length 530;
Best Local Similarity 70.4%; Pred. No. 6.4e-35;
Matches 76; Conservative 13; Mismatches 19; Indels 0; Gaps 0;

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Qy	1	LSFDPPFYGHPLROITTIATGGFIEMGDVIERMLTATOVVAPLMAENPGYSDNSTVVYFD	60
Db	161	LSFDPPFYGHPLNEVTATGGFIYIGEVVHRMLTATQIIAPLMAFDFSVSRNSTVRYFD	220
Qy	61	NGTVFVVQWDHYYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPE	108
Db	221	NGTALVVQWDHVLQDNVNLGSFTFQATLLMDGRIIFGYKEIPVLVTQ	268

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Job time : 41.7978 secs